

## SEARCH REQUEST FORM

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Date: \_\_\_\_\_ Phone: \_\_\_\_\_ Art Unit: \_\_\_\_\_

**Search Topic:**

Please write a detailed statement of search topic. Describe specifically as possible the subject matter to be searched. Define any terms that may have a special meaning. Give examples or relevant citations, authors keywords, etc., if known. For sequences, please attach a copy of the sequence. You may include a copy of the broadest and/or most relevant claim(s).

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## Search Site

\_\_\_\_\_ STIC

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## Type of Search

\_\_\_\_\_ N.A. Sequence

\_\_\_\_\_ A.A. Sequence

\_\_\_\_\_ Structure

\_\_\_\_\_ Bibliographic

## Vendors

\_\_\_\_\_ IG Suite

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\_\_\_\_\_ Other

GenCore version 5.1.3  
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OM protein - protein search, using sw model

Run on: December 4, 2002, 10:06:40 ; Search time 42 Seconds

(without alignments)  
1817.919 Million cell updates/sec

Title: US-09-869-877-10

Sequence: 1 QQSCTFSPNRACWTDGYDIN.....KSDSLKRWVEGEMLYKA 573

Scoring table:

BLOSUM62  
Gapop 10.0 , Gapept 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database :

1: A\_Geneseq\_101002:\*  
2: /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1980.DAT:\*  
3: /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1981.DAT:\*  
4: /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1982.DAT:\*  
5: /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1983.DAT:\*  
6: /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1984.DAT:\*  
7: /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1985.DAT:\*  
8: /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1986.DAT:\*  
9: /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1987.DAT:\*  
10: /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1988.DAT:\*  
11: /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1989.DAT:\*  
12: /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1990.DAT:\*  
13: /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1991.DAT:\*  
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15: /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1993.DAT:\*  
16: /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1994.DAT:\*  
17: /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1995.DAT:\*  
18: /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1996.DAT:\*  
19: /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1997.DAT:\*  
20: /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1998.DAT:\*  
21: /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1999.DAT:\*  
22: /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA2000.DAT:\*  
23: /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA2001.DAT:\*  
24: /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA2002.DAT:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	3158	100.0	573	AAW76315	Myceoliophthora the
2	3158	100.0	573	AAW59913	Myceoliophthora the
3	3158	100.0	573	AAW62503	Myceoliophthora the
4	3158	100.0	573	AAW51782	Myceoliophthora the
5	3158	100.0	573	AAW63124	Myceoliophthora the
6	3158	100.0	573	AAW91085	Myceoliophthora the
7	3158	100.0	620	AAW85500	Myceoliophthora lac
8	3158	100.0	620	AAW16302	Myceoliophthora lac
9	3158	100.0	620	AAW50729	M. thermophila lac
10	3140	99.4	573	AAW79079	Myceoliophthora the

11	3124	98.9	620	AAW19855	Myceoliophthora the
12	3118	98.7	573	AAW76317	Myceoliophthora the
13	3118	98.7	573	AAW79078	Myceoliophthora the
14	3112	98.5	573	AAW76316	Myceoliophthora the
15	3112	98.5	573	AAW79077	Myceoliophthora the
16	2428.5	76.9	623	AAW76464	Melanocarpus albon
17	2096.5	66.4	616	AAW18060	Scybalidium thermo
18	2076.5	65.8	616	AAW76314	Scybalidium thermo
19	2076.5	65.8	616	AAW59915	Scybalidium thermo
20	2076.5	65.8	616	AAW62502	Scybalidium thermo
21	2076.5	65.8	616	AAW51783	Scybalidium thermo
22	2076.5	65.8	616	AAW91086	Scybalidium thermo
23	1071.5	33.9	581	AAW76443	Novel Botrytis cin
24	638	20.2	499	AAW76295	Polyporus pinus
25	636	20.1	499	AAW76295	Polyporus pinus
26	636	20.1	499	AAW60875	Polyporus pinus
27	636	20.1	520	AAW90721	Polyporus pinus
28	636	20.1	520	ABW77510	Laccase-LCC1. Pol
29	635	20.1	499	AAW76297	Trametes versicolo
30	630	19.9	499	AAW76296	Polyporus pinus
31	629	19.9	499	AAW76298	Polyporus pinus
32	620.5	19.6	518	AAW61387	Schizophyllum comm
33	615	19.5	499	AAW7069	Phenol oxidase (PO
34	614	19.4	499	AAW05279	Amino acid sequenc
35	614	19.4	499	AAW07068	Phenol oxidase (PO
36	614	19.4	539	AAW17973	Coprinus cinereus
37	614	19.4	539	AAW76281	Coprinus cinereus
38	614	19.4	539	AAW60874	Coprinus cinereus
39	611.5	19.4	524	AAW92810	Coprinus cinereus
40	609.5	19.3	529	AAW76310	T. versicolor lacc
41	609.5	19.3	529	AAW60878	Rhizoctonia solani
42	609.5	19.3	529	AAW50728	R. solani laccase
43	607.5	19.2	529	AAW16301	Rhizoctonia solani
44	603.5	19.1	529	AAW72328	Laccase R51ac3. R
45	601.5	19.0	511	AAW90724	Laccase-LCC4. Pol

#### ALIGNMENTS

RESULT 1	AAW76315 standard; protein: 573 AA.
ID	AAW76315
XX	AAW76315:
AC	08-JAN-1999 (first entry)
XX	Myceoliophthora thermophila laccase protein.
XX	Laccase; variant; oxidation; dye transfer inhibition; bleaching;
KW	denim; lignin modification; paper strengthening; phenol polymerisation;
KW	hair dye; waste water treatment.
XX	Myceoliophthora thermophila.
OS	Myceoliophthora thermophila.
XX	WO9838287-A1.
PN	03-SEP-1998.
XX	23-FEB-1998: 98WO-DK00070.
PD	28-FEB-1997: 97DK-0000222.
XX	(NOVO ) NOVO-NORDISK AS.
PA	Svendsen A, Xu F;
XX	WPI; 1998-495393/42.
PI	New variants of Coprinus and related laccases with increased
XX	oxidation potential - or altered pH optimum, or mediator or
PT	oxygen-hydroxide ion pathways, useful for oxidation, for inhibiting
XX	

QY 481 LPAFGWVYLSFRADNGALFHCHTAMHYSGLGWYLLERADDLRGAVSDADADLDRLC 540  
 DB 481 LPAFGWVYLSFRADNGALFHCHTAMHYSGLGWYLLERADDLRGAVSDADADLDRLC 540  
 QY 541 ADMRRYPTNPYPKSDSGLKHRRVGECEWLYAKA 573  
 DB 541 ADMRRYPTNPYPKSDSGLKHRRVGECEWLYAKA 573

RESULT 3  
 AAM62503  
 ID AAM62503 standard; Protein; 573 AA.  
 AC AAM62503;  
 XX 09-NOV-1998 (first entry)  
 DT Myceliophthora thermophila laccase.  
 XX  
 XX Coprinus laccase-like enzyme; enzyme engineering; enzyme stability;  
 KM detergent; bleaching.  
 XX  
 OS Myceliophthora thermophila.  
 XX  
 FH Key  
 FT Misc-difference 433  
 FT Location/Qualifiers  
 FT Phe, Trp, Gly, Ser, Thr, Cys, Tyr, Asn,  
 FT Gln, Asp, Glu, Lys, Arg or His (preferably  
 FT Phe, Val, Ile, Leu or Gln) at this  
 FT position  
 FT Misc-difference 373  
 FT "variant may have Ala, Val, Leu, Ile, Pro,  
 FT Phe, Met, Gly, Ser, Thr, Cys, Tyr, Asn,  
 FT Gln, Asp, Glu, Lys, Arg or His (preferably  
 FT Phe or His) at this position"  
 FT Misc-difference 136  
 FT "variant may have Ala, Val, Leu, Ile, Pro,  
 FT Phe, Met, Gly, Ser, Thr, Cys, Tyr, Asn,  
 FT Gln, Asp, Glu, Lys, Arg or His (preferably  
 FT Phe or His) at this position"  
 FT Misc-difference 145  
 FT "variant may have Ala, Val, Leu, Ile, Pro,  
 FT Phe, Trp, Gly, Ser, Thr, Cys, Tyr, Asn,  
 FT Gln, Asp, Glu, Lys, Arg or His (preferably  
 FT Phe or His) at this position"  
 FT Misc-difference 480  
 FT "variant may have Ala, Val, Leu, Ile, Pro,  
 FT Phe, Trp, Gly, Ser, Thr, Cys, Tyr, Asn,  
 FT Gln, Asp, Glu, Lys, Arg or His (preferably  
 FT Phe, Val, Ile, Leu or Gln) at this  
 FT position"  
 FT Misc-difference 137  
 FT "variant may have Ala, Val, Leu, Ile, Pro,  
 FT Phe, Trp, Gly, Ser, Thr, Cys, Met, Asn,  
 FT Gln, Asp, Glu, Lys, Arg or His (preferably  
 FT Phe) at this position"  
 FT Misc-difference 176  
 FT "variant may have Ala, Val, Leu, Ile, Pro,  
 FT Phe, Trp, Gly, Ser, Thr, Cys, Met, Asn,  
 FT Gln, Asp, Glu, Lys, Arg or His (preferably  
 FT Phe) at this position"  
 FT Misc-difference 254  
 FT "variant may have Ala, Val, Leu, Ile, Pro,  
 FT Phe, Trp, Gly, Ser, Thr, Cys, Tyr, Asn,  
 FT Gln, Asp, Glu, Lys, Arg or His (preferably  
 FT Phe, Val, Ile, Leu or Gln) at this  
 FT position"  
 FT W09827198-AL.  
 XX  
 XX PD 25-JUN-1998.

XX 16-DEC-1997; 97WO-DK00571.  
 XX  
 PF 08-SEP-1997; 97DK-0001021.  
 PR 19-DEC-1996; 96DK-0001449.  
 XX  
 PA (NOVO) NOVO-NORDISK AS.  
 XX  
 XX Cherry JR, Pedersen AH, Rasmussen G, Schneider P;  
 PI Svendsen A;  
 DR WPI; 1998-362768/31.  
 XX  
 XX New laccase variants with improved stability - having amino acid  
 PT changes based on Coprinus laccase structure, used for e.g.  
 PT oxidation, dye transfer inhibition or bleaching  
 XX  
 PS Claim 18; 156-157; 168pp; English.  
 XX  
 CC This is a laccase enzyme of Myceliophthora thermophila. The  
 CC invention relates to the design of new variants of Coprinus-like  
 CC laccases (see AAM60874-79, AAM60925 and AAM62501-03); this M.  
 CC thermophila laccase shows 56.5% homology to C. cinereus laccase. The  
 CC modifications are based on the previously unknown three-dimensional  
 CC structure of C. cinereus laccase. Amino acid residues identified as  
 CC being important to protein stability are identified and altered to  
 CC improve stability. The variants are typically obtained by  
 CC mutagenesis of laccase DNA and expression in a host cell. Variants  
 CC are preferably modified within 15 (especially 10 or 5) Angstrom  
 CC of a copper ion in the three-dimensional structure of the laccase.  
 CC For M. thermophila laccase variants, preferred substitutions are  
 CC one or more of W433F/V/I/L/Q, W373F/H, W136F/H, Y145F,  
 CC M480F/V/I/L/Q, Y137F, Y176F and M254F/V/I/L/Q. The stabilised  
 CC laccase variants can be used in detergent additives, for dye  
 CC transfer inhibition in detergents, in bleaching of textiles (in  
 CC particular denim), for lignin modification, paper strengthening,  
 CC phenol polymerisation, hair dyeing and in waste water treatment.  
 XX

Sequence 573 AA:  
 QY Query Match 100.0%; Score 3158; DB 19; Length 573;  
 Best local Similarity 100.0%; Pred. No. 7.6e-276;  
 Matches 573; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QOSCNTPSNACWTDGIDITDYEVDSPDTGVVRYPTLLTLEVDNMTGPGGVYKEMVLY 60  
 DB 1 QOSCNTPSNACWTDGIDITDYEVDSPDTGVVRYPTLLTLEVDNMTGPGGVYKEMVLY 60

QY 61 NNSIIGPTFADMGDITQVIVINNLETNGSIHHMGLHOKGTNLHDANGITTECPPIPKG 120  
 DB 61 NNSIIGPTFADMGDITQVIVINNLETNGSIHHMGLHOKGTNLHDANGITTECPPIPKG 120

QY 121 GRRVYRFAKQOYGTSMYSHFSAOYNGVGAIOINGPASPYPDTDGVPEISDYSSA 180  
 DB 121 GRRVYRFAKQOYGTSMYSHFSAOYNGVGAIOINGPASPYPDTDGVPEISDYSSA 180

QY 122 GRRVYRFAKQOYGTSMYSHFSAOYNGVGAIOINGPASPYPDTDGVPEISDYSSA 180  
 DB 122 GRRVYRFAKQOYGTSMYSHFSAOYNGVGAIOINGPASPYPDTDGVPEISDYSSA 180

QY 181 DELVELTKNSGAPSDNVYLFNGTAKHPEEGEGERANYTLTPGRRRLRLINTSVENHOV 240  
 DB 181 DELVELTKNSGAPSDNVYLFNGTAKHPEEGEGERANYTLTPGRRRLRLINTSVENHOV 240

QY 181 DELVELTKNSGAPSDNVYLFNGTAKHPEEGEGERANYTLTPGRRRLRLINTSVENHOV 240  
 DB 181 DELVELTKNSGAPSDNVYLFNGTAKHPEEGEGERANYTLTPGRRRLRLINTSVENHOV 240

QY 241 SLVNHMCIITAAAMPVFNATVDSLFLFGVGORVDVYEARTPEKNYFNTFGGGLCGG 300  
 DB 241 SLVNHMCIITAAAMPVFNATVDSLFLFGVGORVDVYEARTPEKNYFNTFGGGLCGG 300

QY 241 SLVNHMCIITAAAMPVFNATVDSLFLFGVGORVDVYEARTPEKNYFNTFGGGLCGG 300  
 DB 241 SLVNHMCIITAAAMPVFNATVDSLFLFGVGORVDVYEARTPEKNYFNTFGGGLCGG 300

QY 301 SRNPYPAIFHYAGAGPPTDEGKAPVNDNCIDLPMLKBPVAVDVLGSPAKRADNTLD 360  
 DB 301 SRNPYPAIFHYAGAGPPTDEGKAPVNDNCIDLPMLKBPVAVDVLGSPAKRADNTLD 360

QY 301 SRNPYPAIFHYAGAGPPTDEGKAPVNDNCIDLPMLKBPVAVDVLGSPAKRADNTLD 360  
 DB 301 SRNPYPAIFHYAGAGPPTDEGKAPVNDNCIDLPMLKBPVAVDVLGSPAKRADNTLD 360

QY 361 VTLDITGTPLFPVKKVNGSAINIDMGRAVDYVLTQNTSFPFGYIVIVEVNGADQSYLIE 420  
 DB 361 VTLDITGTPLFPVKKVNGSAINIDMGRAVDYVLTQNTSFPFGYIVIVEVNGADQSYLIE 420

QY 361 VTLDITGTPLFPVKKVNGSAINIDMGRAVDYVLTQNTSFPFGYIVIVEVNGADQSYLIE 420  
 DB 361 VTLDITGTPLFPVKKVNGSAINIDMGRAVDYVLTQNTSFPFGYIVIVEVNGADQSYLIE 420

QY 421 NDGAPFTLPHPHLGHDFYVILGRSPDESASNERHVFPARDAGLLSGANPVRDYSM 480  
 DB 421 NDGAPFTLPHPHLGHDFYVILGRSPDESASNERHVFPARDAGLLSGANPVRDYSM 480

XX AAM63124;  
 AC 12-OCT-1998 (first entry)  
 DT  
 XX Myceliophthora thermophila laccase protein.  
 DE  
 XX Laccase protein; variant; lignin modification; paper strengthening;  
 KM dye transfer inhibition; phenol2 polymerisation; hair dyeing;  
 KM textile bleaching; denim; waste water treatment.  
 XX  
 OS Myceliophthora thermophila.  
 FH  
 XX Key Location/Qualifiers  
 PN W09827197-A1.  
 PD 25-JUN-1998.  
 XX  
 PF 12-DEC-1997; 97WO-DK00566.  
 XX  
 PR 08-SEP-1997; 97DK-0001020.  
 XX 19-DEC-1996; 96DK-0001450.  
 XX  
 PA (NOVO) NOVO-NORDISK AS.  
 XX  
 PI Cherry JR, Pedersen AH, Rasmussen G, Schneider P;  
 PI Svendsen A;  
 DR WPI; 1998-362767/31.  
 XX  
 XX New laccase variants - have amino acid changes in Myceliophthora or  
 PT Scybalidium laccase(s), used for e.g. oxidation, dye transfer  
 PT Inhibition or bleaching  
 PS  
 XX Claim 1: Pages 18-21; 30pp; English.  
 CC The present sequence represents a laccase protein. The sequence is used  
 CC to construct laccase variants (AAM63124-27, AAM63129-32 and AAM63135),  
 CC which have improved stability as compared to the parent laccase, and  
 CC comprises a mutation in tyrosine, tryptophan or methionine residues. The  
 CC laccase variants can be used for e.g. lignin modification, paper  
 CC strengthening, dye transfer inhibition in detergents, phenol  
 CC polymerisation, hair dyeing, bleaching of textiles (in particular  
 CC bleaching of denim) and waste water treatment.  
 CC  
 SQ Sequence 573 AA;  
 Query Match 100.0%; Score 3158; DB 19; Length 573;  
 Best Local Similarity 100.0%; Pred. No. 7, 6e-276;  
 Matches 573; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 301 SRNPYPAIFHYAGAPGPPTEGKAPVDHNCIDLPLNLFKVVAVDVLGFAKRAADNTLD 360  
 QY 361 VTIDTTGTPLFWKVKVNSAINIDWGRAVDYVLTQNTSPFPQNIIVEANQADMSYLLIE 420  
 DB 361 VTIDTTGTPLFWKVKVNSAINIDWGRAVDYVLTQNTSPFPQNIIVEANQADMSYLLIE 420  
 QY 421 NDGAPFTPLPHMLHGHDFYVLTGRSPESPASNERHVEDPARDAGLLSGANPYRDVSM 480  
 DB 421 NDGAPFTPLPHMLHGHDFYVLTGRSPESPASNERHVEDPARDAGLLSGANPYRDVSM 480  
 QY 481 LPAFGWVLSFRADNPGAMLFHCHIAMHVSGLGVYLTFRADDLRGAVSADADDLRLC 540  
 DB 481 LPAFGWVLSFRADNPGAMLFHCHIAMHVSGLGVYLTFRADDLRGAVSADADDLRLC 540  
 QY 541 ADMRRYPTNPYPKSDGKLRHVEEGEWLYKA 573  
 DB 541 ADMRRYPTNPYPKSDGKLRHVEEGEWLYKA 573  
 RESULT 6  
 AAY91085  
 ID AAY91085 standard; protein; 573 AA.  
 XX  
 AC AAY91085;  
 XX  
 DT 13-SEP-2000 (first entry)  
 XX  
 DE Myceliophthora thermophila laccase amino acid sequence SEQ ID NO:1.  
 XX  
 KM Laccase; polyphenol oxidase; oxidation; mutant; variant; detergent;  
 KM inhibiting dye transfer; bleaching textile; lignin modification;  
 KM paper strengthening; phenol polymerisation; hair dyeing;  
 KM waste water treatment.  
 XX  
 OS Thielavia heteroythallica.  
 XX  
 PN US6060442-A.  
 XX  
 PD 09-MAY-2000.  
 XX  
 PF 24-FEB-1998; 98US-0028887.  
 XX  
 PR 24-FEB-1998; 98US-0028887.  
 XX  
 PA (NOVO) NOVO-NORDISK AS.  
 XX  
 PI Svendsen A;  
 XX  
 DR WPI; 2000-375259/32.  
 XX  
 PT Laccase variants for oxidizing substrate, inhibiting dye transfer and  
 PT bleaching textiles has increased oxidation potential and/or changed pH  
 PT and/or altered mediatory and/or altered oxygen/hydroxyl group pathways  
 PT  
 PS Claim 1: Column 9-12; 10pp; English.  
 XX  
 XX The present invention describes laccase variants (1S) with increased  
 CC oxidation potential and/or changed pH optimum and/or altered mediator  
 CC pathway and/or altered O2/OH- pathway. Also described are: (1) a  
 CC detergent additive comprising (1) in the form of a non-dusting granule,  
 CC a stabilised liquid or a protected enzyme; and (2) a detergent  
 CC composition comprising (1) and a surfactant. (1) is useful for oxidising  
 CC a substrate, inhibiting dye transfer and bleaching textiles. 1S are also  
 CC useful for various industrial applications such as lignin modification,  
 CC paper strengthening, phenol polymerisation, hair dyeing and waste water  
 CC treatment. The present sequence represents the Myceliophthora thermophila  
 CC (also known as Thielavia heteroythallica) laccase amino acid sequence  
 CC which is modified in the exemplification of the present invention.  
 CC  
 SQ Sequence 573 AA;





SO Sequence 573 AA:

Query Match 99.4%; Score 3140; DB 19; Length 573;  
 Best Local Similarity 99.5%; Pred. No. 3.2e-274;  
 Matches 570; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 1 QOSCTPSNRACWTDGYDINTDYEDSPDTGVRRPTTLTLEVDNMTGPGVYKEKVMY 60  
 DB 1 QOSCTPSNRACWTDGYDINTDYEDSPDTGVRRPTTLTLEVDNMTGPGVYKEKVMY 60  
 OY 61 NNSIIGPTIFADMGDTIQVTVINLETNGTSIHMHGKHOKGTLHKGANGITECP1PPKG 120  
 DB 61 NNSIIGPTIFADMGDTIQVTVINLETNGTSIHMHGKHOKGTLHKGANGITECP1PPKG 120  
 OY 121 GRKYRFRKAQOYGTSMYSHSFSAOYGNVYGAIQINGPASLPYDLDGVFPISDYYSSA 180  
 DB 121 GRKYRFRKAQOYGTSMYSHSFSAOYGNVYGAIQINGPASLPYDLDGVFPISDYYSSA 180  
 OY 181 DELVELTKNSGAPESDNYLFNGTAKHPETGESEYANVTLPGRHRRLRLINTSVENHFQY 240  
 DB 181 DELVELTKNSGAPESDNYLFNGTAKHPETGESEYANVTLPGRHRRLRLINTSVENHFQY 240  
 OY 241 SLVNHNTMCIADAMVPVNAATVDSLEFLVGORVDVIEANRTPGNVFWNTFGGGLCG 300  
 DB 241 SLVNHNTMCIADAMVPVNAATVDSLEFLVGORVDVIEANRTPGNVFWNTFGGGLCG 300  
 OY 301 SRNPYPAAIFHYAGAGGPPTEDEGKAPVDHNCIDLPNLKPVYARVPLSGFAKRAADNTLD 360  
 DB 301 SRNPYPAAIFHYAGAGGPPTEDEGKAPVDHNCIDLPNLKPVYARVPLSGFAKRAADNTLD 360  
 OY 361 VTLDTGTPLFWKYNKSAINIDMGRAVVDVYLQNTSPPGNIYEVGAQOMSWTLE 420  
 DB 361 VTLDTGTPLFWKYNKSAINIDMGRAVVDVYLQNTSPPGNIYEVGAQOMSWTLE 420  
 OY 421 NDPGAFETLPHPMHLGHDFYVLGRSPDESPASNERHVEDPAPADAGLLSGANVPRDYSK 480  
 DB 421 NDPGAFETLPHPMHLGHDFYVLGRSPDESPASNERHVEDPAPADAGLLSGANVPRDYSK 480  
 OY 481 LPAFGVVVLSFRADNPGAMLFHCHIAHVSGLGVYLLERADDLRGAVSDADADDLRLC 540  
 DB 481 LPAFGVVVLSFRADNPGAMLFHCHIAHVSGLGVYLLERADDLRGAVSDADADDLRLC 540  
 OY 541 ADMRRYWPNTNPPYKSDSGLKHRRVGECEWLYKA 573  
 DB 541 ADMRRYWPNTNPPYKSDSGLKHRRVGECEWLYKA 573

RESULT 11  
 AAM19855  
 ID AAM19855 standard; Protein; 620 AA.  
 AC AAM19855;  
 AC AAM19855;  
 DT 11-SEP-1997 (first entry)  
 DE Mycellophthora thermophila laccase useful in dye composition.  
 KW Laccase; dye; keratin; hair; fur; hide; wool.  
 OS Mycellophthora thermophila.  
 XX WO9719999-A1.  
 XX 05-JUN-1997.  
 XX 29-NOV-1996; 96WO-DK00499.  
 XX 30-NOV-1995; 95DK-0001357.  
 XX (NOVO ) NOVO-NORDISK AS.  
 XX Aaslyng D, Rorbaek K, Sorensen NH;

DR WPI: 1997-310565/28.  
 DR N-PSDB; AAT72106.  
 XX Dyeing composition for dyeing keratinous fibres, e.g. human hair. -  
 PT comprises microbial laccase, dye precursor and optionally a modifier  
 XX Disclosure: Page 19-22; 37pp; English.  
 PS  
 CC Mycellophthora thermophila laccase (AAM19855) catalyses the  
 CC oxidation of phenols, resulting in the prod. of aryloxy-radical  
 CC intermediates. The ultimate coupling of these intermediates  
 CC provides a combination of dimeric, oligomeric and polymeric  
 CC reaction products, some of which can be used to form dyes. The  
 CC enzyme can be produced in heterologous host cells, esp. filamentous  
 CC fungi, yeast or bacteria, utilising vectors contg. the laccase gene  
 CC (AAT72106). It is used in compositions, together with one or more  
 CC dye precursors and optionally one or more modifiers, for dyeing  
 CC fur, hide, wool and hair, esp. human hair. Dyeing is faster.  
 CC and/or requires less enzyme and/or less precursor (some precursors  
 CC are unhealthy and carcinogenic) than prior methods using oxidising  
 CC enzyme and precursor.  
 CC  
 SO Sequence 620 AA:

Query Match 98.8%; Score 3124; DB 18; Length 620;  
 Best Local Similarity 98.8%; Pred. No. 1e-272;  
 Matches 566; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

OY 1 QOSCTPSNRACWTDGYDINTDYEDSPDTGVRRPTTLTLEVDNMTGPGVYKEKVMY 60  
 DB 48 QOSCTPSNRACWTDGYDINTDYEDSPDTGVRRPTTLTLEVDNMTGPGVYKEKVMY 107  
 OY 61 NNSIIGPTIFADMGDTIQVTVINLETNGTSIHMHGKHOKGTLHKGANGITECP1PPKG 120  
 DB 108 NNSIIGPTIFADMGDTIQVTVINLETNGTSIHMHGKHOKGTLHKGANGITECP1PPKG 167  
 OY 121 GRKYRFRKAQOYGTSMYSHSFSAOYGNVYGAIQINGPASLPYDLDGVFPISDYYSSA 180  
 DB 168 GRKYRFRKAQOYGTSMYSHSFSAOYGNVYGAIQINGPASLPYDLDGVFPISDYYSSA 227  
 OY 181 DELVELTKNSGAPESDNYLFNGTAKHPETGESEYANVTLPGRHRRLRLINTSVENHFQY 240  
 DB 228 DELVELTKNSGAPESDNYLFNGTAKHPETGESEYANVTLPGRHRRLRLINTSVENHFQY 287  
 OY 241 SLVNHNTMCIADAMVPVNAATVDSLEFLVGORVDVIEANRTPGNVFWNTFGGGLCG 300  
 DB 288 SLVNHNTMCIADAMVPVNAATVDSLEFLVGORVDVIEANRTPGNVFWNTFGGGLCG 347  
 OY 301 SRNPYPAAIFHYAGAGGPPTEDEGKAPVDHNCIDLPNLKPVYARVPLSGFAKRAADNTLD 360  
 DB 348 SRNPYPAAIFHYAGAGGPPTEDEGKAPVDHNCIDLPNLKPVYARVPLSGFAKRAADNTLD 407  
 OY 361 VTLDTGTPLFWKYNKSAINIDMGRAVVDVYLQNTSPPGNIYEVGAQOMSWTLE 420  
 DB 408 VTLDTGTPLFWKYNKSAINIDMGRAVVDVYLQNTSPPGNIYEVGAQOMSWTLE 467  
 OY 421 NDPGAFETLPHPMHLGHDFYVLGRSPDESPASNERHVEDPAPADAGLLSGANVPRDYSK 480  
 DB 468 NDPGAFETLPHPMHLGHDFYVLGRSPDESPASNERHVEDPAPADAGLLSGANVPRDYSK 527  
 OY 481 LPAFGVVVLSFRADNPGAMLFHCHIAHVSGLGVYLLERADDLRGAVSDADADDLRLC 540  
 DB 528 LPAFGVVVLSFRADNPGAMLFHCHIAHVSGLGVYLLERADDLRGAVSDADADDLRLC 587  
 OY 541 ADMRRYWPNTNPPYKSDSGLKHRRVGECEWLYKA 573  
 DB 588 ADMRRYWPNTNPPYKSDSGLKHRRVGECEWLYKA 620

RESULT 12  
 AAM76317  
 ID AAM76317 standard; protein; 573 AA.

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XX 20-FEB-1998; 98WO-DK00067.
XX 28-FEB-1997; 97DK-0000221.
XX (NOVO ) NOVO-NORDISK AS.
XX
XX Svendsen A;
XX WPI; 1998-495392/42.
XX
XX New variants of laccase with increased oxidation potential - or
XX altered pH optimum, mediator efficiency or oxygen-hydroxide ion
XX pathways, useful for oxidation, inhibiting dye transfer and in
XX textile bleaching
XX
XX Claim 4; Page -: 34pp; English.
XX
XX The laccase protein mutants AAW79077-W79079 contain one or more of the
XX above mutations and are examples of polypeptides modified from the
XX valid-type sequence by using site-directed, random, or localised random
XX mutagenesis. These mutants may have an (a) increased oxidation
XX potential, (b) altered pH optimum, (c) altered mediator efficiency, (d)
XX altered oxygen/hydroxide ion pathway, depending on the particular
XX mutations that have occurred. This particular sequence has mutations
XX that will alter the laccase's oxygen/hydrogen ion pathway. These
XX variants can be used to oxidise substrates, inhibit dye transfer, as
XX detergent additives and bleaching textiles. They can also be used in
XX lignin modification; strengthening paper; polymerisation of phenols;
XX dyeing of hair and textiles and waste water treatment.
XX N.B. This sequence is not shown in the specification but is derived
XX from the wild-type Mycellophthora thermophila laccase sequence given in
XX the specification.
XX
XX Sequence 573 AA;
XX
XX Query Match 98.7%; Score 3118; DB 19; Length 573;
XX Best Local Similarity 99.0%; Pred. No 3.1e-272;
XX Matches 567; Conservative 1; Mismatches 5; Indels 0; Gaps 0;
XX
XX 1 QOQSCNTPSNRACWTDGYDINTDYEVDSPDTGVNRYTLTLEVDNMTGPDGVNKKVWLV 60
XX 1 QOQSCNTPSNRACWTDGYDINTDYEVDSPDTGVNRYTLTLEVDNMTGPDGVNKKVWLV 60
XX
XX 61 NNSITGPTIRADMGDTQOVYVINLFTNGTSIHNGHLQKNTLNHOGANGTTECPPIPKG 120
XX 61 NNSITGPTIRADMGDTQOVYVINLFTNGTSIHNGHLQKNTLNHOGANGTTECPPIPKG 120
XX
XX 121 GRKYRREKAOQYGTSMWHSFSAQYNGVYGAIDINGPASLPYDTDLGVPFISDYSSA 180
XX 121 GRKYRREKAOQYGTSMWHSFSAQYNGVYGAIDINGPASLPYDTDLGVPFISDYSSA 180
XX
XX 121 GRKYRREKAOQYGTSMWHSFSAQYNGVYGAIDINGPASLPYDTDLGVPFISDYSSA 180
XX 121 GRKYRREKAOQYGTSMWHSFSAQYNGVYGAIDINGPASLPYDTDLGVPFISDYSSA 180
XX
XX 181 DELVELTKNSGAPPSDNLVFNKGAKHETGEGEYANTLPGRRHRLRLINTSVENHEOV 240
XX 181 DELVELTKNSGAPPSDNLVFNKGAKHETGEGEYANTLPGRRHRLRLINTSVENHEOV 240
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XX 181 DELVELTKNSGAPPSDNLVFNKGAKHETGEGEYANTLPGRRHRLRLINTSVENHEOV 240
XX 181 DELVELTKNSGAPPSDNLVFNKGAKHETGEGEYANTLPGRRHRLRLINTSVENHEOV 240
XX
XX 241 SLVNHPTCIIAAMVPVNAFTVDSLELGVGQRDVYVEANRFGNRYFNVTGGGLCGG 300
XX 241 SLVNHPTCIIAAMVPVNAFTVDSLELGVGQRDVYVEANRFGNRYFNVTGGGLCGG 300
XX
XX 241 SLVNHPTCIIAAMVPVNAFTVDSLELGVGQRDVYVEANRFGNRYFNVTGGGLCGG 300
XX 241 SLVNHPTCIIAAMVPVNAFTVDSLELGVGQRDVYVEANRFGNRYFNVTGGGLCGG 300
XX
XX 301 SRNPYPAIRFHYAGAPGPTDEGKAPVDHNCIDLPLKRPVADVPLSGFAKADNTLD 360
XX 301 SRNPYPAIRFHYAGAPGPTDEGKAPVDHNCIDLPLKRPVADVPLSGFAKADNTLD 360
XX
XX 301 SRNPYPAIRFHYAGAPGPTDEGKAPVDHNCIDLPLKRPVADVPLSGFAKADNTLD 360
XX 301 SRNPYPAIRFHYAGAPGPTDEGKAPVDHNCIDLPLKRPVADVPLSGFAKADNTLD 360
XX
XX 361 VTLDTGTGTPLEFVKVNSAINDMGRAVDVYLTQNTSPFPGYNIIVEVNGADQMSYMLIE 420
XX 361 VTLDTGTGTPLEFVKVNSAINDMGRAVDVYLTQNTSPFPGYNIIVEVNGADQMSYMLIE 420
XX
XX 361 VTLDTGTGTPLEFVKVNSAINDMGRAVDVYLTQNTSPFPGYNIIVEVNGADQMSYMLIE 420
XX 361 VTLDTGTGTPLEFVKVNSAINDMGRAVDVYLTQNTSPFPGYNIIVEVNGADQMSYMLIE 420
XX
XX 421 NDGAPFTLPHRNHLGHNDYVLGRSPDESASNERHVFPRPARAGLLSGANPRRDVSE 480
XX 421 NDGAPFTLPHRNHLGHNDYVLGRSPDESASNERHVFPRPARAGLLSGANPRRDVSE 480
XX
XX 421 NDGAPFTLPHRNHLGHNDYVLGRSPDESASNERHVFPRPARAGLLSGANPRRDVSE 480
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XX 481 LPAFGWVLSFRADNPGAWLFHCHIAWHVSGGLGVYLERADDLRGAVSDADADDLRLC 540
XX 481 LPAFGWVLSFRADNPGAWLFHCHIAWHVSGGLGVYLERADDLRGAVSDADADDLRLC 540
XX

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DB 481 LPAFGWVLSFRADNPGAWLFHCHIAWHVSGGLGVYLERADDLRGAVSDADADDLRLC 540
XX
XX 541 ADMRRYPTNPYPKSDSGLKHWRVEGEWLVKA 573
XX 541 ADMRRYPTNPYPKSDSGLKHWRVEGEWLVKA 573
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XX 541 ADMRRYPTNPYPKSDSGLKHWRVEGEWLVKA 573
XX 541 ADMRRYPTNPYPKSDSGLKHWRVEGEWLVKA 573
XX
XX RESULT 14
XX AAW76316
XX ID AAW76316 standard; protein: 573 AA.
XX
XX AC AAW76316;
XX
XX 08-JAN-1999 (first entry)
XX
XX Mycellophthora thermophila laccase protein variant.
XX
XX Laccase; variant; oxidation; dye transfer inhibition; bleaching;
XX denim; lignin modification; paper strengthening; phenol polymerisation;
XX hair dye; waste water treatment.
XX
XX Synthetic.
XX Mycellophthora thermophila.
XX
XX Key Location/Qualifiers
XX FT Misc-difference 106 /label- D106X
XX FT /note- "X is optionally Ala, Val, Pro, Leu, Ile,
XX FT Phe, Tyr or Trp"
XX
XX FT Misc-difference 108 /label- A108X
XX FT /note- "X is optionally Val, Pro, Leu, Ile,
XX FT Phe, Tyr, or Trp"
XX
XX FT Misc-difference 109 /label- N109X
XX FT /note- "X is optionally Ala, Val, Pro, Leu, Ile,
XX FT Phe, Tyr, Gln or Trp"
XX
XX FT Misc-difference 428 /label- T428X
XX FT /note- "X is optionally Ala, Val, Pro, Leu, Ile,
XX FT Phe, Tyr or Trp"
XX
XX FT Misc-difference 500 /label- L500X
XX FT /note- "X is optionally Ile, Phe, Tyr, or Trp"
XX
XX FT Misc-difference 510 /label- S510X
XX FT /note- "X is optionally Ala, Val, Pro, Leu, Ile,
XX FT Phe, Tyr or Trp"
XX
XX FT Misc-difference 511 /label- G511X
XX FT /note- "X is optionally Ala, Val, Pro, Leu, Ile,
XX FT Phe, Tyr or Trp"
XX
XX FT Misc-difference 514 /label- G514X
XX FT /note- "X is optionally Ala, Val, Pro, Leu, Ile,
XX FT Phe, Tyr, or Trp"
XX
XX W09838287-A1.
XX
XX 03-SEP-1998.
XX
XX 23-FEB-1998; 98WO-DK00070.
XX
XX 28-FEB-1997; 97DK-0000222.
XX
XX (NOVO ) NOVO-NORDISK AS.
XX
XX Svendsen A, Xu F;
XX
XX WPI; 1998-495393/42.
XX
XX New variants of Coprinus and related laccases with increased

```

Query Match 98.5%; Score 3112; DB 19; Length 573;  
Best Local Similarity 98.6%; Pred. No. 1,1e-271;  
Matches 565; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

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DB 1 QOSCNTPSNRACWTDGYDINTDEYDSDPTGVVRPYTLTLEVDNMTGPDGVYKEKMYLV 60
QY 61 NNSIIGPTIFADMGDTIQYTVINNTETNGTSIMHGLHOKGTNLHDGANGITECPPIPKG 120
DB 61 NNSIIGPTIFADMGDTIQYTVINNTETNGTSIMHGLHOKGTNLHDGANGITECPPIPKG 120
QY 121 GRKVRFEKAOQGTSMWHSFSAOYNGNGVGAIOIINGPASLPRDNLGVPISDYYSYA 180
DB 121 GRKVRFEKAOQGTSMWHSFSAOYNGNGVGAIOIINGPASLPRDNLGVPISDYYSYA 180
QY 181 DELVELTKNSGAPFSDNVLFNGTAKHPEGESEYANVTLPGRHRRLRLINTSVENHFOY 240
DB 181 DELVELTKNSGAPFSDNVLFNGTAKHPEGESEYANVTLPGRHRRLRLINTSVENHFOY 240
QY 241 SLVNHNTMCIIAADNVPVNMATVDSLELGVGQRYDVVIEANRTPGNYMFNVTEGGGLCGG 300
DB 241 SLVNHNTMCIIAADNVPVNMATVDSLELGVGQRYDVVIEANRTPGNYMFNVTEGGGLCGG 300
QY 301 SRNPYPALFHHYAGAPGPGPTDEGKAPVDHNCIDLPLKPYVAROYPLSGFAKRAADNTLD 360
DB 301 SRNPYPALFHHYAGAPGPGPTDEGKAPVDHNCIDLPLKPYVAROYPLSGFAKRAADNTLD 360
QY 361 VTLDTGTPLFVWKNGSAINIDMGRAVDYVLTONTSPPGYNIVEVNGADOMSYLIE 420
DB 361 VTLDTGTPLFVWKNGSAINIDMGRAVDYVLTONTSPPGYNIVEVNGADOMSYLIE 420
QY 421 NDPGAPFTLPHPMHLGHDFYVLGRSPDES PASNERHVPDPARADGLLSGANVRRDYSM 480
DB 421 NDPGAPFTLPHPMHLGHDFYVLGRSPDES PASNERHVPDPARADGLLSGANVRRDYSM 480
QY 481 LPAFGWVYLSFRADNPGAVLFHCHITAMHVSGLGVYTLERADDLRGAVSDADADDLRLC 540
DB 481 LPAFGWVYLSFRADNPGAVLFHCHITAMHVSGLGVYTLERADDLRGAVSDADADDLRLC 540
QY 541 ADMRRYWPNTNPPYKSDSGLKHHRVVEGGEWLKRA 573
DB 541 ADMRRYWPNTNPPYKSDSGLKHHRVVEGGEWLKRA 573
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Search completed: December 4, 2002, 10:46:25  
Job time : 44 secs

GenCore version 5.1.3  
Copyright (c) 1993 - 2002 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: December 4, 2002, 10:46:31 ; Search time 17 Seconds

(without alignments)  
991.726 Million cell updates/sec

Title: US-09-869-877-10

Perfect score: 3158

Sequence: 1 QOQCNTPSNRACWTDGTYDIN.....KSDGLKRWVEGEWLVKA 573

Scoring table: BLOSUM62

Searched: 262574 segs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :  
1: Issued Patents.AA.\*  
2: /cgn2\_6/ptodata/1/1aa/5A.COMB.pep.\*  
3: /cgn2\_6/ptodata/1/1aa/5B.COMB.pep.\*  
4: /cgn2\_6/ptodata/1/1aa/6A.COMB.pep.\*  
5: /cgn2\_6/ptodata/1/1aa/6B.COMB.pep.\*  
6: /cgn2\_6/ptodata/1/1aa/BACKFILES1.pep.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3158	100.0	573	2	US-08-991-531-1
2	3158	100.0	573	2	US-09-032-315-10
3	3158	100.0	573	2	US-08-993-318A-10
4	3158	100.0	573	3	US-09-028-887-1
5	3158	100.0	573	4	US-09-399-886-10
6	3158	100.0	573	4	US-09-396-260-10
7	3158	100.0	573	4	US-09-518-901-1
8	3158	100.0	573	4	US-09-576-281-10
9	3158	100.0	620	1	US-08-706-037-27
10	3158	100.0	620	2	US-09-005-397-27
11	3158	100.0	620	5	PCT-US95-06815-2
12	3127	99.0	620	1	US-08-940-661A-2
13	3127	99.0	620	2	US-09-083-485-2
14	3127	99.0	620	2	US-08-939-218A-2
15	2089.5	66.2	616	1	US-08-749-882A-2
16	2089.5	66.2	616	2	US-08-539-114-2
17	2084.5	66.0	616	5	PCT-US95-06816-2
18	2076.5	65.8	616	2	US-08-991-531-2
19	2076.5	65.8	616	2	US-09-032-315-9
20	2076.5	65.8	616	3	US-08-993-318A-9
21	2076.5	65.8	616	4	US-09-028-887-2
22	2076.5	65.8	616	4	US-09-399-886-9
23	2076.5	65.8	616	4	US-09-396-260-9
24	2076.5	65.8	616	4	US-09-518-901-2
25	2076.5	65.8	616	4	US-09-576-281-9
26	636	20.1	499	2	US-09-032-315-2
27	636	20.1	499	2	US-08-993-318A-2

28	636	20.1	499	4	US-09-399-886-2	Sequence 2, Appli
29	636	20.1	499	4	US-09-396-260-2	Sequence 2, Appli
30	636	20.1	499	4	US-09-576-281-2	Sequence 2, Appli
31	636	20.1	520	1	US-08-462-484-2	Sequence 2, Appli
32	636	20.1	520	1	US-08-441-147-2	Sequence 2, Appli
33	636	20.1	520	5	PCT-US95-07536-2	Sequence 2, Appli
34	614	19.4	539	2	US-09-032-315-1	Sequence 1, Appli
35	614	19.4	539	3	US-08-689-421-27	Sequence 1, Appli
36	614	19.4	539	4	US-08-993-318A-1	Sequence 27, Appli
37	614	19.4	539	4	US-09-399-886-1	Sequence 1, Appli
38	614	19.4	539	4	US-09-396-260-1	Sequence 1, Appli
39	614	19.4	539	4	US-09-389-528-27	Sequence 27, Appli
40	614	19.4	539	4	US-09-181-827A-27	Sequence 27, Appli
41	614	19.4	539	4	US-09-576-281-1	Sequence 1, Appli
42	609.5	19.3	529	1	US-08-172-331B-14	Sequence 14, Appli
43	609.5	19.3	529	1	US-08-706-037-25	Sequence 25, Appli
44	609.5	19.3	529	2	US-09-005-397-25	Sequence 25, Appli
45	609.5	19.3	529	2	US-09-032-315-5	Sequence 5, Appli

## ALIGNMENTS

RESULT 1  
US-08-991-531-1  
; Sequence 1, Application US/08991531  
; Patent No. 5925554  
; GENERAL INFORMATION:

APPLICANT: Pedersen, Anders Hjelholt  
APPLICANT: Svendsen, Allan  
APPLICANT: Schneider, Palle  
APPLICANT: Rasmussen, Grethe  
APPLICANT: Cherry, Joel  
TITLE OF INVENTION: Myceliophthora And Scytalidium laccase  
TITLE OF INVENTION: Variants  
NUMBER OF SEQUENCES: 2  
CORRESPONDENCE ADDRESS:  
ADDRESS: No. 59255540 No. 5925554disk of No. 5925554th America, Inc.  
STREET: 405 Lexington Avenue  
CITY: New York  
STATE: NY

COUNTRY: USA  
ZIP: 10174  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FASTSEQ for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/991,531  
FILING DATE: 16-DEC-1997  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Rozek, Carol  
REGISTRATION NUMBER: 36,993  
REFERENCE/DOCKET NUMBER: 5125, 200-US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 212-867-0123  
TELEFAX: 212-878-9655

INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 573 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-991-531-1

Query Match 100.0%; Score 3158; DB 2; Length 573;  
Best Local Similarity 100.0%; Pred. No. 3.6e-290;  
Matches 573; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QOQCNTPSNRACWTDGTYDINIDYEVDSPTGCVVRPYTLILEVDNMWGTGPDGVYKRVMLV 60

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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/993,318A
FILING DATE: December 18, 1997
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Gregg, Valeta A.
REGISTRATION NUMBER: 33,728
REFERENCE/DOCKET NUMBER: 5032.200-US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-867-0123
TELEFAX: 212-878-9655
TELEX:
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 573 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-993-318A-10

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Query Match          100.0%; Score 3158; DB 2; Length 573;
Best Local Similarity 100.0%; Pred. No. 3.6e-290;
Matches 573; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 QOSCTPSNRACWTGDIINTDYEVDSPTGVRRPYTLTLEVDNMTGPDGVYKEKMYLV 60
DB 1 QOSCTPSNRACWTGDIINTDYEVDSPTGVRRPYTLTLEVDNMTGPDGVYKEKMYLV 60
QY 61 NNSIIGPTIFADMGDTIOYVINNLETNGTSIMHGLHOKGTNLHDGANGITECP1PPKG 120
DB 61 NNSIIGPTIFADMGDTIOYVINNLETNGTSIMHGLHOKGTNLHDGANGITECP1PPKG 120
QY 121 GKKVYRFAKQOYGTSMYHSHFSAQYGNVGAQIINGPASPDPDOLGVPIISDYSSA 180
DB 121 GKKVYRFAKQOYGTSMYHSHFSAQYGNVGAQIINGPASPDPDOLGVPIISDYSSA 180
QY 181 DELVELTKNSGAPFSDNVLENGTAKHPEGEGETYANVTLPGRHRRLRLINTSVENHFQY 240
DB 181 DELVELTKNSGAPFSDNVLENGTAKHPEGEGETYANVTLPGRHRRLRLINTSVENHFQY 240
QY 241 SLVNHHTMCIIAADMPVNAATVDSLEFLGVGORYDVYIEANRTPGNVFNTEFGGLICGG 300
DB 241 SLVNHHTMCIIAADMPVNAATVDSLEFLGVGORYDVYIEANRTPGNVFNTEFGGLICGG 300
QY 301 SRNPYPALIFHYAGAPGPTDEGKAPVDHNCIDLPLKPVYADVPLSGFAKRAADNTLD 360
DB 301 SRNPYPALIFHYAGAPGPTDEGKAPVDHNCIDLPLKPVYADVPLSGFAKRAADNTLD 360
QY 361 VILDTTGTPLFVWKVNGSAINIDMGRAVVDYVLTQNTSFPFGNIVIVNGADQMSYWLIE 420
DB 361 VILDTTGTPLFVWKVNGSAINIDMGRAVVDYVLTQNTSFPFGNIVIVNGADQMSYWLIE 420
QY 421 NDPGAPFTLPHPMHLGHDFYVLGRSPDESPPASNERHVPFPDADAGLLSGANPYRQVSM 480
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QY 481 LPAFGWVVLSEFRADNPGAMLFCHITAMHVSGLGVYLLERADDLRGAVSDADADDLRLC 540
DB 481 LPAFGWVVLSEFRADNPGAMLFCHITAMHVSGLGVYLLERADDLRGAVSDADADDLRLC 540
QY 541 ADMRRYWPNTNPPKSDSGLKHRRVGEEMLVKA 573
DB 541 ADMRRYWPNTNPPKSDSGLKHRRVGEEMLVKA 573

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RESULT 4
US-09-028-887-1
; Sequence 1, Application us/09028887
; Patent No. 6060442

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GENERAL INFORMATION:
APPLICANT: Svendsen, Allan
TITLE OF INVENTION: LACCASE MUTANTS
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSER: No. 6060442o No. 6060442disk of No. 6060442th America
STREET: 405 Lexington Avenue
CITY: New York
STATE: NY
COUNTRY: USA
ZIP: 10174
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/028,887
FILING DATE: 24-February-1998
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Gregg, Valeta A.
REGISTRATION NUMBER: 35,127
REFERENCE/DOCKET NUMBER: 5201.200-US
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 573 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-028-887-1

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Query Match          100.0%; Score 3158; DB 3; Length 573;
Best Local Similarity 100.0%; Pred. No. 3.6e-290;
Matches 573; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

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QY 1 QOSCTPSNRACWTGDIINTDYEVDSPTGVRRPYTLTLEVDNMTGPDGVYKEKMYLV 60
DB 1 QOSCTPSNRACWTGDIINTDYEVDSPTGVRRPYTLTLEVDNMTGPDGVYKEKMYLV 60
QY 61 NNSIIGPTIFADMGDTIOYVINNLETNGTSIMHGLHOKGTNLHDGANGITECP1PPKG 120
DB 61 NNSIIGPTIFADMGDTIOYVINNLETNGTSIMHGLHOKGTNLHDGANGITECP1PPKG 120
QY 121 GKKVYRFAKQOYGTSMYHSHFSAQYGNVGAQIINGPASPDPDOLGVPIISDYSSA 180
DB 121 GKKVYRFAKQOYGTSMYHSHFSAQYGNVGAQIINGPASPDPDOLGVPIISDYSSA 180
QY 181 DELVELTKNSGAPFSDNVLENGTAKHPEGEGETYANVTLPGRHRRLRLINTSVENHFQY 240
DB 181 DELVELTKNSGAPFSDNVLENGTAKHPEGEGETYANVTLPGRHRRLRLINTSVENHFQY 240
QY 241 SLVNHHTMCIIAADMPVNAATVDSLEFLGVGORYDVYIEANRTPGNVFNTEFGGLICGG 300
DB 241 SLVNHHTMCIIAADMPVNAATVDSLEFLGVGORYDVYIEANRTPGNVFNTEFGGLICGG 300
QY 301 SRNPYPALIFHYAGAPGPTDEGKAPVDHNCIDLPLKPVYADVPLSGFAKRAADNTLD 360
DB 301 SRNPYPALIFHYAGAPGPTDEGKAPVDHNCIDLPLKPVYADVPLSGFAKRAADNTLD 360
QY 361 VILDTTGTPLFVWKVNGSAINIDMGRAVVDYVLTQNTSFPFGNIVIVNGADQMSYWLIE 420
DB 361 VILDTTGTPLFVWKVNGSAINIDMGRAVVDYVLTQNTSFPFGNIVIVNGADQMSYWLIE 420
QY 421 NDPGAPFTLPHPMHLGHDFYVLGRSPDESPPASNERHVPFPDADAGLLSGANPYRQVSM 480
DB 421 NDPGAPFTLPHPMHLGHDFYVLGRSPDESPPASNERHVPFPDADAGLLSGANPYRQVSM 480
QY 481 LPAFGWVVLSEFRADNPGAMLFCHITAMHVSGLGVYLLERADDLRGAVSDADADDLRLC 540
DB 481 LPAFGWVVLSEFRADNPGAMLFCHITAMHVSGLGVYLLERADDLRGAVSDADADDLRLC 540

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Db 1 QOQSCNTPSRNACWTDGDIINTDIEVDSPDGVRRPTLLTLEVDNMTGPDGVYKEKVMY 60
QY 61 NNSIIGPTIFADMGDTIOYTVINNLETNGTSIMHGLHOKGTMLHDGANGITECP1PPKG 120
DB 61 NNSIIGPTIFADMGDTIOYTVINNLETNGTSIMHGLHOKGTMLHDGANGITECP1PPKG 120
QY 121 GKRVRFKAQOYGTSMYHSHFSAQYNGVGAIOINGPASLPYDTDLGVFPISDYSSA 180
DB 121 GKRVRFKAQOYGTSMYHSHFSAQYNGVGAIOINGPASLPYDTDLGVFPISDYSSA 180
QY 181 DELVELTKNSGAFSDNVLFNGTAKHPEEGEYANVTLLPGRRHRLRLINTSVENHFOY 240
DB 181 DELVELTKNSGAFSDNVLFNGTAKHPEEGEYANVTLLPGRRHRLRLINTSVENHFOY 240
QY 241 SLVNHMTCTIADMVNMTVDLSFLVGORVDVYIEANRPFGNFWNTFEGGILLCG 300
DB 241 SLVNHMTCTIADMVNMTVDLSFLVGORVDVYIEANRPFGNFWNTFEGGILLCG 300
QY 301 SRNPYPALFHYAGAPGPTDEGKAPVDHNCIDLPLNLRPVARVDPLSGFAKADNTLD 360
DB 301 SRNPYPALFHYAGAPGPTDEGKAPVDHNCIDLPLNLRPVARVDPLSGFAKADNTLD 360
QY 361 VTLDTGTGLEFWKVGSAINIDMGRAVVDYVLTQNTSEPPGNIYEVGADQMSYWLIE 420
DB 361 VTLDTGTGLEFWKVGSAINIDMGRAVVDYVLTQNTSEPPGNIYEVGADQMSYWLIE 420
QY 421 NDGPAPFTLPHPMHLHGHPYVYLGSRPDESPASNERHVEDPADAGILLSGANVRDYSK 480
DB 421 NDGPAPFTLPHPMHLHGHPYVYLGSRPDESPASNERHVEDPADAGILLSGANVRDYSK 480
QY 481 LPAFGWVLSFRADNGAMLFCHIAMHVSGLGVYLLERADDLRGAVSDADADDLRLC 540
DB 481 LPAFGWVLSFRADNGAMLFCHIAMHVSGLGVYLLERADDLRGAVSDADADDLRLC 540
QY 541 ADMRRYPTNPYPKSDSGLKHRRVEEGEWLVKA 573
DB 541 ADMRRYPTNPYPKSDSGLKHRRVEEGEWLVKA 573

RESULT 7
US-09-518-901-1
; Sequence 1, Application US/09518901
; Patent No. 6218170
; GENERAL INFORMATION:
; APPLICANT: Svendsen, Allan
; TITLE OF INVENTION: LACCASE MUTANTS
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 62181700 No. 6218170disk of No. 6218170th America
; STREET: 405 Lexington Avenue
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10174
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/518, 901
; FILING DATE: 06-Mar-2000
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/028, 887
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Gregg, Valeta A.
; REGISTRATION NUMBER: 35,127
; REFERENCE/DOCKET NUMBER: 5201.200-US
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:

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; LENGTH: 573 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-518-901-1

Query Match 100.0%; Score 3158; DB 4; Length 573;
Best Local Similarity 100.0%; Pred. No. 3,6e-290;
Matches 573; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QOQSCNTPSRNACWTDGDIINTDIEVDSPDGVRRPTLLTLEVDNMTGPDGVYKEKVMY 60
DB 1 NNSIIGPTIFADMGDTIOYTVINNLETNGTSIMHGLHOKGTMLHDGANGITECP1PPKG 60
QY 61 NNSIIGPTIFADMGDTIOYTVINNLETNGTSIMHGLHOKGTMLHDGANGITECP1PPKG 120
DB 61 NNSIIGPTIFADMGDTIOYTVINNLETNGTSIMHGLHOKGTMLHDGANGITECP1PPKG 120
QY 121 GKRVRFKAQOYGTSMYHSHFSAQYNGVGAIOINGPASLPYDTDLGVFPISDYSSA 180
DB 121 GKRVRFKAQOYGTSMYHSHFSAQYNGVGAIOINGPASLPYDTDLGVFPISDYSSA 180
QY 181 DELVELTKNSGAFSDNVLFNGTAKHPEEGEYANVTLLPGRRHRLRLINTSVENHFOY 240
DB 181 DELVELTKNSGAFSDNVLFNGTAKHPEEGEYANVTLLPGRRHRLRLINTSVENHFOY 240
QY 241 SLVNHMTCTIADMVNMTVDLSFLVGORVDVYIEANRPFGNFWNTFEGGILLCG 300
DB 241 SLVNHMTCTIADMVNMTVDLSFLVGORVDVYIEANRPFGNFWNTFEGGILLCG 300
QY 301 SRNPYPALFHYAGAPGPTDEGKAPVDHNCIDLPLNLRPVARVDPLSGFAKADNTLD 360
DB 301 SRNPYPALFHYAGAPGPTDEGKAPVDHNCIDLPLNLRPVARVDPLSGFAKADNTLD 360
QY 361 VTLDTGTGLEFWKVGSAINIDMGRAVVDYVLTQNTSEPPGNIYEVGADQMSYWLIE 420
DB 361 VTLDTGTGLEFWKVGSAINIDMGRAVVDYVLTQNTSEPPGNIYEVGADQMSYWLIE 420
QY 421 NDGPAPFTLPHPMHLHGHPYVYLGSRPDESPASNERHVEDPADAGILLSGANVRDYSK 480
DB 421 NDGPAPFTLPHPMHLHGHPYVYLGSRPDESPASNERHVEDPADAGILLSGANVRDYSK 480
QY 481 LPAFGWVLSFRADNGAMLFCHIAMHVSGLGVYLLERADDLRGAVSDADADDLRLC 540
DB 481 LPAFGWVLSFRADNGAMLFCHIAMHVSGLGVYLLERADDLRGAVSDADADDLRLC 540
QY 541 ADMRRYPTNPYPKSDSGLKHRRVEEGEWLVKA 573
DB 541 ADMRRYPTNPYPKSDSGLKHRRVEEGEWLVKA 573

RESULT 8
US-09-576-281-10
; Sequence 10, Application US/09576281
; Patent No. 6277611
; GENERAL INFORMATION:
; APPLICANT: Pedersen, Anders
; TITLE OF INVENTION: LACCASE MUTANTS
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 62776110 No. 6277611disk of No. 6277611th America
; STREET: 405 Lexington Avenue
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10174
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk

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Db 408 VILDTGTPLFWKVGSAINIDMGRAVVDYLTONTSPPGYNIVEVNGADQMSYWLIE 467  
Qy 421 NDGAPFTLPHPMHLGHDFYVYGRSPDESPASNERHVEDPADACILSGANFVRDYSM 480  
Db 468 NDGAPFTLPHPMHLGHDFYVYGRSPDESPASNERHVEDPADACILSGANFVRDYSM 527  
Qy 481 LPAFGVVLSPFADNPGAMLFHCHIAMHVSGLGVYTLERADDLRGAVSDADADDLRLC 540  
Db 528 LPAFGVVLSPFADNPGAMLFHCHIAMHVSGLGVYTLERADDLRGAVSDADADDLRLC 587  
Qy 541 ADMRRYPTNPYPKSDSGLKHRRVGEGLVKA 573  
Db 588 ADMRRYPTNPYPKSDSGLKHRRVGEGLVKA 620  
RESULT 10  
US-09-005-397-27  
Sequence 27, Application US/09005397  
Patent No 5972670  
GENERAL INFORMATION:  
APPLICANT: Xu, Feng  
APPLICANT: Berka, Randy M.  
APPLICANT: Wahleithner, Jill A.  
TITLE OF INVENTION: BLUE COPPER OXIDASE MUTANTS WITH  
TITLE OF INVENTION: ENHANCED ACTIVITY  
NUMBER OF SEQUENCES: 29  
CORRESPONDENCE ADDRESS:  
ADDRESS: No. 59726700 No. 5972670disk of No. 5972670th America, Inc.  
STREET: 405 Lexington Avenue, 64th floor  
CITY: New York  
STATE: New York  
COUNTRY: United States of America  
ZIP: 10174-6401  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/005,397  
CLASSIFICATION:  
FILING DATE:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/706,037  
FILING DATE: 30-AUG-1996  
APPLICATION NUMBER: US 60/002,800  
FILING DATE: 1-SEP-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Harrington, James J.  
REGISTRATION NUMBER: 38,711  
REFERENCE/DOCKET NUMBER: 4526, 200-US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 212-867-0123  
TELEFAX: 212-878-9655  
INFORMATION FOR SEQ ID NO: 27:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 620 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-09-005-397-27  
Query Match 100.0%; Score 3158; DB 2; Length 620;  
Best Local Similarity 100.0%; Pred. No. 4e-290;  
Matches 573; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 108 NSIIGPTIFADMGDTIQVTVINLETNGTSHHMGHLOKGTNLHDGANGITECPPIPKG 167  
Qy 121 GRKYRFAKQOYCTSWYSHSFSAOYNGVYGAIOINGPASTLPYDTLGVPIIDYYS 180  
Db 168 GRKYRFAKQOYCTSWYSHSFSAOYNGVYGAIOINGPASTLPYDTLGVPIIDYYS 227  
Qy 181 DELVELTKNSGAFESDNVLENGTAKHPEEGEYANVTLPGRHRLRLINTSVENHFOY 240  
Db 228 DELVELTKNSGAFESDNVLENGTAKHPEEGEYANVTLPGRHRLRLINTSVENHFOY 287  
Qy 241 SLVNHMCIIADMPVNMATVDSLFLVGQRVDVYTEANRTGNTWENTFEGGLCG 300  
Db 288 SLVNHMCIIADMPVNMATVDSLFLVGQRVDVYTEANRTGNTWENTFEGGLCG 347  
Qy 301 SRNPYPAIFHYAGAPGPTDEGKAPVDHNCIDLNLKPVYADVPISGFARADNTLD 360  
Db 348 SRNPYPAIFHYAGAPGPTDEGKAPVDHNCIDLNLKPVYADVPISGFARADNTLD 407  
Qy 361 VILDTGTPLFWKVGSAINIDMGRAVVDYLTONTSPPGYNIVEVNGADQMSYWLIE 420  
Db 408 VILDTGTPLFWKVGSAINIDMGRAVVDYLTONTSPPGYNIVEVNGADQMSYWLIE 467  
Qy 421 NDGAPFTLPHPMHLGHDFYVYGRSPDESPASNERHVEDPADACILSGANFVRDYSM 480  
Db 468 NDGAPFTLPHPMHLGHDFYVYGRSPDESPASNERHVEDPADACILSGANFVRDYSM 527  
Qy 481 LPAFGVVLSPFADNPGAMLFHCHIAMHVSGLGVYTLERADDLRGAVSDADADDLRLC 540  
Db 528 LPAFGVVLSPFADNPGAMLFHCHIAMHVSGLGVYTLERADDLRGAVSDADADDLRLC 587  
Qy 541 ADMRRYPTNPYPKSDSGLKHRRVGEGLVKA 573  
Db 588 ADMRRYPTNPYPKSDSGLKHRRVGEGLVKA 620  
RESULT 11  
PCT-US95-06815-2  
Sequence 2, Application PC/TUS9506815  
GENERAL INFORMATION:  
APPLICANT:  
APPLICANT:  
TITLE OF INVENTION: PURIFIED MYCELIOPTHORA LACCASES AND NUCLEIC  
NUMBER OF SEQUENCES: 2  
TITLE OF INVENTION: ACIDS ENCODING SAME  
CORRESPONDENCE ADDRESS:  
ADDRESS: Novo Nordisk of North America, Inc.  
STREET: 405 Lexington Avenue, Suite 6400  
COUNTRY: U.S.A.  
ZIP: 10174-6401  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US95/06815  
FILING DATE: 31-May-1995  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/253,781  
FILING DATE: 03-June-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Lowmey, Karen A.  
REGISTRATION NUMBER: 31,274  
REFERENCE/DOCKET NUMBER: 4184, 204-WO  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 212 867 0298  
TELEFAX: 212 867 0298  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 620 amino acids  
TYPE: amino acid  
STRANDEDNESS: single



Sequence 2, Application US/09083485  
Patent No. 5948121  
GENERAL INFORMATION:  
APPLICANT: Dorrit Aaslyng  
APPLICANT: Sorensen, Niels H.  
TITLE OF INVENTION: Laccases with Improved Dyeing  
NUMBER OF SEQUENCES: 2  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: No. 5948121 of No. 5948121 of No. 5948121 of America, Inc.  
STREET: 405 Lexington Avenue  
CITY: New York  
STATE: NY  
COUNTRY: USA  
ZIP: 10174  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSO for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/083.485  
FILING DATE: 20-MAY-1998  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Gregg, Valeta  
REGISTRATION NUMBER: 35,127  
REFERENCE/DOCKET NUMBER: 4639, 204-US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 212-867-0123  
TELEFAX: 212-878-9655  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 620 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-09-083-485-2

Query Match 99.0%; Score 3127; DB 2; Length 620;  
Best Local Similarity 99.0%; Pred. No. 3.5e-287;  
Matches 567; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

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QY 181 DELVELTKNSGAPSDVNLFGTAKHRETGEFANVTLTGRRRLRLINTSVENHFOV 240  
DB 228 DELVELTKNSGAPSDVNLFGTAKHRETGEFANVTLTGRRRLRLINTSVENHFOV 287  
QY 241 SLVNHWTICIIAADVVPVNAATVDSLFLGVGORYVTEANRTPGNYMNTVEGGGLCG 300  
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QY 301 SRNPYPAIFHYAGAPGPTDEGKAPVDHNCIDLPLKPYVARDVPLSGFAKRAADNTLD 360  
DB 348 SRNPYPAIFHYAGAPGPTDEGKAPVDHNCIDLPLKPYVARDVPLSGFAKRAADNTLD 407  
QY 361 VTLDGTETPLFVWKVNSAINIIMGRVVDVLTQNTSEPPGYNIVENYNGADQSYWLE 420  
DB 408 VTLDGTETPLFVWKVNSAINIIMGRVVDVLTQNTSEPPGYNIVENYNGADQSYWLE 467  
QY 421 NDBGAPFTLPHPMHLHGHDFVILGRSPDESPASNERHVFDPARDAAGLLSGANPRADVS 480  
DB 468 NDBGAPFTLPHPMHLHGHDFVILGRSPDESPASNERHVFDPARDAAGLLSGANPRADVS 527

QY 481 LPAGWVVLSEFADNPGAMLFCHIAHVSGLGVYLERADDLRGAVSDADADDLRLC 540  
DB 528 LPAGWVVLSEFADNPGAMLFCHIAHVSGLGVYLERADDLRGAVSDADADDLRLC 587  
QY 541 ADMRRYPTNPKSDSGLKRHWYEGEWLVKA 573  
DB 588 ADMRRYPTNPKSDSGLKRHWYEGEWLVKA 620

RESULT 14  
US-08-939-218A-2  
Sequence 2, Application US/08939218A  
Patent No. 5981243  
GENERAL INFORMATION:  
APPLICANT: BERKA, Randy Michael  
APPLICANT: BROWN, Stephen H.  
APPLICANT: XU, Peng  
APPLICANT: SCHNEIDER, Palle  
APPLICANT: OXENB LL, Karen M.  
TITLE OF INVENTION: PURIFIED MYCELIOPHTHORA LACCASES AND NUCLEIC  
NUMBER OF SEQUENCES: 2  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: No. 5981243 of No. 5981243 of No. 5981243 of America, Inc.  
STREET: 405 Lexington Avenue, 64th floor  
CITY: New York  
STATE: New York  
COUNTRY: United States of America  
ZIP: 10174-6401  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/939, 218A  
FILING DATE: 29-SEPT-1997  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Rozek, Carol E.  
REGISTRATION NUMBER: 36,993  
REFERENCE/DOCKET NUMBER: 4184, 120-US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 212-867-0123  
TELEFAX: 212-878-9655  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 620 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-939-218A-2

Query Match 99.0%; Score 3127; DB 2; Length 620;  
Best Local Similarity 99.0%; Pred. No. 3.5e-287;  
Matches 567; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

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DB 48 QOSCNTPSNRACWTDGDIINTDYEVSDPDGVVPRYTLTLEVDNMTGPDGVYVEKWL 107  
QY 61 NNSIIGPTIFADMGDTIQVYINNLETNGTSHHGHGLOKGTNLHDGANGITECPPIPKG 120  
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DB 168 GRKYRREKAAQOYGTSMYSHESAQYGNVGAIOINGPASLPYDTDLGVPFISDYSSA 227  
QY 181 DELVELTKNSGAPSDVNLFGTAKHRETGEFANVTLTGRRRLRLINTSVENHFOV 240

GenCore version 5.1.3  
Copyright (c) 1993 - 2002 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: December 4, 2002, 10:47:46 ; Search time 12 Seconds  
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Title: US-09-869-877-10  
Perfect score: 3158  
Sequence: 1 QOSCNTPSNRACWTDGYDIN.....KSDSGIKHRWVEGEMLYKA 573

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 103943 seqs, 16242309 residues  
Total number of hits satisfying chosen parameters: 103943

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database: Published Applications RA.\*  
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2: /cgn2\_6/ptodata/1/pubppa/PCT\_NEW\_PUB.pep.\*  
3: /cgn2\_6/ptodata/1/pubppa/US06\_NEW\_PUB.pep.\*  
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8: /cgn2\_6/ptodata/1/pubppa/US08\_NEW\_PUB.pep.\*  
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13: /cgn2\_6/ptodata/1/pubppa/US60\_PUBCOMB.pep.\*  
14: /cgn2\_6/ptodata/1/pubppa/US60\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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2	2076.5	65.8	616	10	US-09-732-350-9 Sequence 9, Appl
3	636	20.1	499	10	US-09-732-350-2 Sequence 2, Appl
4	614	19.4	539	10	US-09-732-350-1 Sequence 1, Appl
5	609.5	19.3	529	10	US-09-732-350-5 Sequence 5, Appl
6	571	18.1	499	10	US-09-732-350-3 Sequence 3, Appl
7	565	17.9	572	10	US-09-732-350-7 Sequence 7, Appl
8	557.5	17.7	575	10	US-09-732-350-8 Sequence 8, Appl
9	556	17.6	548	10	US-09-732-350-4 Sequence 4, Appl
10	542	17.2	599	10	US-09-732-350-6 Sequence 6, Appl
11	446	14.1	564	9	US-09-944-160-12 Sequence 12, Appl
12	241	7.6	583	9	US-09-942-185-2 Sequence 2, Appl
13	204	6.5	572	9	US-09-942-185-4 Sequence 4, Appl
14	198	6.3	568	12	US-10-080-233-4 Sequence 4, Appl
15	197	6.2	594	10	US-09-338-723A-2 Sequence 2, Appl
16	197	6.2	594	12	US-10-080-210-2 Sequence 2, Appl
17	197	6.2	594	10	US-10-080-233-2 Sequence 2, Appl
18	195.5	6.2	627	10	US-09-338-723A-4 Sequence 4, Appl
19	195.5	6.2	627	12	US-10-080-210-4 Sequence 4, Appl

20	195.5	6.2	627	12	US-10-080-210-7 Sequence 7, Appl
21	120.5	3.8	545	10	US-09-988-200-8 Sequence 8, Appl
22	101.5	3.2	1016	12	US-10-007-693-95 Sequence 95, Appl
23	101	3.2	1260	9	US-10-024-918-27 Sequence 27, Appl
24	101	3.2	1477	9	US-10-092-880-4 Sequence 4, Appl
25	99	3.1	404	10	US-09-815-242-11242 Sequence 11242, A
26	98	3.1	522	12	US-10-090-624-4 Sequence 4, Appl
27	97	3.1	821	9	US-09-764-868-883 Sequence 883, App
28	96.5	3.1	485	9	US-09-918-543-2 Sequence 2, Appl
29	96.5	3.1	485	10	US-09-769-864-1 Sequence 7, Appl
30	96.5	3.1	485	10	US-09-854-346-2 Sequence 2, Appl
31	96.5	3.1	485	10	US-09-902-188A-1 Sequence 1, Appl
32	96.5	3.1	485	10	US-09-833-435A-3 Sequence 13, Appl
33	96.5	3.1	726	10	US-09-833-435A-13 Sequence 8, Appl
34	96.5	3.1	726	10	US-09-841-132-594 Sequence 445, App
35	96	3.0	448	10	US-09-841-132-594 Sequence 594, App
36	96	3.0	1751	10	US-09-841-132-594 Sequence 16, App
37	96	3.0	1751	10	US-09-841-132-594 Sequence 425, App
38	95	3.0	654	12	US-10-090-624-16 Sequence 425, App
39	95	3.0	1184	9	US-09-978-697-425 Sequence 425, App
40	95	3.0	1184	9	US-09-978-697-425 Sequence 425, App
41	95	3.0	1184	9	US-09-978-697-425 Sequence 425, App
42	94.5	3.0	776	10	US-09-833-435A-4 Sequence 4, Appl
43	93.5	3.0	1261	10	US-09-815-242-11963 Sequence 11963, A
44	93	2.9	867	9	US-09-839-894-6 Sequence 6, Appl
45	93	2.9	881	10	US-09-850-351A-32 Sequence 32, Appl

## ALIGNMENTS

RESULT 1  
US-09-732-350-10  
Sequence 10, Application US/09732350  
Patient No. US20010031490A1  
GENERAL INFORMATION:  
APPLICANT: Svendsen, Allan  
APPLICANT: Xu, Feng  
TITLE OF INVENTION: LACCASE MUTANTS  
NUMBER OF SEQUENCES: 10  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: No. US20010031490A10 No. US20010031490A1disk of No. US20010031490A1  
STREET: 405 Lexington Avenue  
CITY: New York  
STATE: NY  
COUNTRY: USA  
ZIP: 10174  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FASTSEQ for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/732.350  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 09/032,315  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Rozek, Carol  
REGISTRATION NUMBER: 36,993  
REFERENCE/DOCKET NUMBER: 5200.200-US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 212-867-0123  
TELEFAX: 212-878-9655  
INFORMATION FOR SEQ ID NO: 10:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 573 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein

ADDRESSEE: No. US20010031490A10 No. US20010031490A1disk of No. US20010031490A1th  
STREET: 405 Lexington Avenue  
CITY: New York  
STATE: NY  
COUNTRY: USA  
ZIP: 10174  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSeq for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/732.350  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 09/032.315  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Rozek, Carol  
REGISTRATION NUMBER: 36,993  
REFERENCE/DOCKET NUMBER: 5200.200-US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 212-867-0123  
TELEFAX: 212-878-9655  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 499 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-09-732-350-2

Query Match 20.1%; Score 636; DB 10; Length 499;  
Best Local Similarity 33.0%; Pred. No. 1.9e-46;  
Matches 184; Conservative 69; Mismatches 204; Indels 100; Gaps 24;

QY 31 GVVREPTLTLEVDNMTGPDGVYKREKVMVNNSSIIIGPTIFADMGDTIQVTVNNLETN-- 88  
DB 3 GPVADLTITNAV-----SPDGFSROAV-VVNGCTPGPLITGNMGDRFQVNTVDNLTNHTM 57  
QY 89 --GTSIHNGHGHOKTNLHDGANGITECPTRPKGGRKYRFRK-QOYGTSWYSHRSAY 145  
DB 58 LKSTSIHNGHGFQKGTNNADGPAFINOCPI-SSGHSFLDFQVDDAGTFWVHSHLSTOY 116  
QY 146 GNGVVAIQI---NGPASIPTYDILG--VFPISDIYSSADELVELTKNSGAPF---SDN 197  
DB 117 CDGLNGPVPVVDNDPAADLYVDNDQVYITLVDTKTHVAA-----KLGPAPFLGADA 168  
QY 198 VLENGTAKHPETGECEYANVTLPGRRRRLRLINTSVENHFOVSLVNTHTCIIAADMPV 257  
DB 169 TLINKGSPSTTTADLSVITPKGRYRFLVSLSCDPNMFSSIDGHNMTIETDSINT 228  
QY 258 NAMVDSLEFLVGORYDYITEANKRPENWF--NTFFGGGLCGGSRNTPPAIFHYAGA 315  
DB 229 APLVYDSIOIFAAORYSFVLEANOAVDNTWMIRANPNFNGVGTGGIN---SAILLYDGA 284  
QY 316 PGGPPT---DEGKAPVDNHCIDLPNLKPYVARDVPLSGFAKRAVDNLTDTGTPLFV 372  
DB 285 AAVEFTTQTSTAP-----LNEVNLHPLVTTAVPGSPVAGVDLAINNAFENNGINFF- 338  
QY 373 WKVNGSAINIIDGRAVVDVYL-TQNTS--FPPG--YNIIVEANGADOMSWYLIENDGAPF 427  
DB 339 --INAGSFPPTVPVPLLOITISGONNODLLPSSGSVSLPS-NADTISFPATAAGCA-- 393  
QY 428 TLPHMHHLGHFFYVLGKSPDESASNERKRVPPADAG--LLSGANPVAROV--SMRPA 463  
DB 394 --PHFPHLEIGHAFAYV-----RSAGSTVYVNNPPIFRDVSSTGTPA 432  
QY 484 FG-WVTVLSFRANPGAMLFHCHTAMVHVSGLGVVYLERADDLGAVSADADADDLRLCAD 542  
DB 433 ACDNVTIRRTDPCGWFHLCHIDFHLBAGFAVVFADIDIVASA----- 477

QY 543 WRRWPTNPRKSDSGL 559  
DB 478 -----NPVPOAWSDL 487

RESULT 4  
US-09-732-350-1  
Sequence 1, Application US/09732350  
Patent No. US20010031490A1  
GENERAL INFORMATION:  
APPLICANT: Svendsen, Allan  
TITLE OF INVENTION: LACCASE MUTANTS  
NUMBER OF SEQUENCES: 10  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: No. US20010031490A10 No. US20010031490A1disk of No. US20010031490A1  
STREET: 405 Lexington Avenue  
CITY: New York  
STATE: NY  
COUNTRY: USA  
ZIP: 10174  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSeq for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/732.350  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 09/032.315  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Rozek, Carol  
REGISTRATION NUMBER: 36,993  
REFERENCE/DOCKET NUMBER: 5200.200-US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 212-867-0123  
TELEFAX: 212-878-9655  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 539 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-09-732-350-1

Query Match 19.4%; Score 614; DB 10; Length 539;  
Best Local Similarity 32.5%; Pred. No. 1.6e-44;  
Matches 174; Conservative 70; Mismatches 204; Indels 88; Gaps 21;

QY 37 TLITFEVDNMTGPDGVYKREKVMVNNSSIIIGPTIFADMGDTIQVTVNNLETN--NGTSI 92  
DB 26 TMLTITNAN--VSPDGTFRGILV--NGVHPLRIGSKNDNFELNVNDNDNPLMRPTSI 81  
QY 93 HNHGLHOKGTNLHDGANGITECPTRPKGGRKYRFR-KAOYGTSWYSHRSAYGNGVVG 151  
DB 82 HNHGLHOKGTNLHDGANGITECPTRPKGGRKYRFR-KAOYGTSWYSHRSAYGNGVVG 140  
QY 152 AIOI---NGPASIPTYDILG--VFPISDIYSSADELVELTKNSGAPFSDNVLFNSTAH 206  
DB 141 PMVITVDNDPMAVLYDEDEENTITLADWYHHPAPSI-----QGAAPDPAFLINKGRY 194  
QY 207 PEGGECEYANVTLPGRRRRLRLINTSVENHFOVSLVNTHTCIIAADMPVNMATVDSLF 266  
DB 195 VGGPAAELSTVNEGCKTKRMLRLISLSCDPNMFSSIDGHNMTIETDSINT 254  
QY 267 LGVGRYDYITEANKRPENWF--TFGGGLCGGSRNTPPAIFHYAGAPGPPDDEG 324  
DB 255 IFTGORYSFVLDANQVDNWTMIRAPNKGKNGLAGTFANGVNSAILRYAGANADPTTSA 314

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; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-732-350-3

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Query Match	Score 571;	DB 10;	Length 499;
18.1%;			
20.7%;			

```

QY PDGVVKEVYVNNVNSIGPTFEADMGTOIVTVNNLETN----GTSHHNGCHQKGTNL 104
  ||| :::: :::: :::: :::: :::: :::: :::: :::: :::: :::: |||
Db PDGSLRDNI-VYVNCVBPSPLTGKKGRFOLYNNVDLTNNISMKLTSHHHGFPQAGTNM 75
  ||| :::: :::: :::: :::: :::: :::: :::: :::: :::: :::: |||
QY HDGANGIIECPTEPKGRKRYFRKA--OQYGTSPYSHSFSAOYNGVYGAIOI---NGPAS 160
  :| :::: :::: :::: :::: :::: :::: :::: :::: :::: :::: :|
Db AEGPAFVNOCTI-ASGHSFLDIEHVPPDQAGTFWHSHSLSTOYCDGLGPRVYVDPKDPHA 134
  :| :::: :::: :::: :::: :::: :::: :::: :::: :::: :::: :|
  76 AEGPAFVNOCTI-ASGHSFLDIEHVPPDQAGTFWHSHSLSTOYCDGLGPRVYVDPKDPHA 134
QY LPVPTD--LGAFPSIDYVYSSADELVETLTKSGAPF---SDNYLFNGSTARKHPETGECEYA 215
  ||| :::: :::: :::: :::: :::: :::: :::: :::: :::: :::: |||
Db SRVDVNESTYITLTDMWHTLA-----RLGKFEFLGADATILINGLSASTPTATALA 166
  ||| :::: :::: :::: :::: :::: :::: :::: :::: :::: :::: |||

```

QY	216	NVTTEPGRRHRLRLINISVENHFEVSLVNHMTCIADNPVNVAWNTTSEFLGQKRYD	275
		: : : : :   : : : : :   : : : : :   : : : : :   : : : : :	
Db	187	VINVHGGRKYRFLVLSIDCPNPTFFSIDGHNLIVIEVDGINSQLPLVDSIQIFAQRYSF	246
QY	276	VIEANRPFGNTWF--NTTFGGLLCGSRNRPRAIRHYAGAPRGSPRTDECKARVDHNCL	333
		: : : : :   : : : : :   : : : : :   : : : : :   : : : : :	
Db	247	VLANNQITGVNTRAPNPFEGTVGFAGGIN---SAILRTGGAIPAAEETTTQTQPSV----	297

[illegible]

Qy	440	FYVLCGRSPDESPASNERHVFEDPADAG--LLSGANPVARYD--SMLEAFG--VWVLSRAD	4444
Db	404	FAYV-----RSAGSTFYNYNDPIFRDVSVCYCPAAGDNVYIRQTD	4444
Qy	495	MPGAMLFHCHTAMHYSGGLSVVYLERADDLGAIVSDADADDLRLCDMKRRYPTNYPRK	554
Db	445	MPGPFLLCHIDHFLDGGFAVLEVEDVAVAA-----NVPVK	482

Qy	555	SDSGL	559
		:	
Db	483	AWSDL	487

RESULT 7  
US-09-732-350-7  
; Sequence 7, Application US/09732350  
; Patent No. US20010031490A1

1 APPLICANT: Svendsen, Allan  
2 APPLICANT: Xu, Feng  
3 TITLE OF INVENTION: LACCASE MUTANTS  
4 NUMBER OF SEQUENCES: 10  
5 CORRESPONDENCE ADDRESS:  
6 ADDRESS: No. US20010031490AIdisk of No. US20010031490AIdisk  
7 STREET: 405 Lexington Avenue

```

; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/032,315
;

```

```

1  ATTORNEY/AGENT INFORMATION:
2  ?
3  ? NAME: Rozek, Carol
4  ?
5  ? REGISTRATION NUMBER: 36,993
6  ?
7  ? REFERENCE/DOCKET NUMBER: 5200.200-US
8  ?
9  ? TELECOMMUNICATION INFORMATION:
10 ?
11 ? TELEPHONE: 212-867-0123
12 ?
13 ? TELEFAX: 212-878-9655
14 ?
15 ? INFORMATION FOR SEQ ID NO: 7:
16 ?
17 ? SEQUENCE CHARACTERISTICS:
18 ?
19 ? LENGTH: 572 amino acids
20 ?
21 ? TYPE: amino acid
22 ?
23 ? STRANDEDNESS: single
24 ?
25 ? TOPOLOGY: linear
26 ?
27 ? MOLECULE TYPE: protein
28 ?
29 ? US-09-732-350-7

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Query Match	17.9%;	Score 565;	DB 10;	Length 572;
Best Local Similarity	31.2%;	Pred. No. 2.6e-40;		
Matches 176;	Conservative 60;	Mismatches 206;	Indels 122;	Gaps 22,

**Oy** 49 PDGVVKEKVMYNNSSIIGPTIFADMGDIQVTYINNLEFN-----GTSIHNGHLHGKGTN 103  
       |||::|||   ||||:||||:||||   |||||||  
**Db** 35 PDGVVERD-ATLVNGGYPGPLIEANKGDGLKKVKYNKL-TNPDMYRTTSHHNGGLQIHRNA 92

```

0y 104 LHDGNGTDECPIDPPKGRKUYRFAAQOYGSYMSHRSADYGVGVAIDINPASPAPY 16
    | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 93 DDDGPAFTQCPIDYVQASUYTMTPLGQDGTGYTWHSHLSQSYVDGSLGSLVLYPKD- PH 15

164 -----DIDDLGVPFISDYYISADELVLTNSCAPSPDNLTNG-----TAKRPET 20
    | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 152 RLKVIDDEKVLIIIGDYHTTSSKAIL-ATNTNITLQOPDASTINGKGRFDDNPAPMNT 210

```

[illegible]

```

Oy  310 FHAYAPGCGPTDEG---KAPVHNCIDLEPNLKRYAD-----VPLS--G 355
Db  327 IKYWKHKHKGRLSSHGGLKARWMEGSLHLGRNDYVRQNETTVVYMDKTKVLRLEHG 380
Oy  351 FA---KADNILDYLD---TTGRLPFWKNG-----SAINDMGAAVVDY 395
Db  387 AACGSKRPADLVLDITGVNFTTGH---WMNLNIDPKSGPDMPTLKLITDTSVSEST 442

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OY      333  LTONTSPFGVYIVVNQADOMSYWLINDGAPRTLLPHNHLIGHDYVL--GRSPDES 455
      : : | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB      443  QPEHIIILPKKNCVBFN-----IKNGSG--LGVIYHPIHLGHTEDVQFGNNPP-- 485
OY      451  PASNERHYVDPARDAGLLSGANPVARVDYSLMPLRGYVYLSRADNPGMLTGHCHIAHYVS 511
      : : | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB      490  -----NYNPPRRDVGATGDEG-VFQKRTDNPAGWELTCHIDIMLE 530

```

Qy	511	GGTGGVYLERADDLRGAVSDAD	534
		:: ::	
Db	531	EGFAMVFAAPAPATKGGPKSVVD	554

GENERAL INFORMATION:  
 ;  
 ; Filing No.: 02-001593-17-001  
 ;  
 ; APPLICANT: Svendsen, Allan  
 ;  
 ; APPLICANT: Xu, Feng

Oy		511	GGLGVYLLERADDLRGAVSDADAD	534
		:	:	:
		:	:	:
		:	:	:
Db		531	EGFAMVFAEAPBAIKGGPKSPVD	554

RESULT 8  
US-09-732-350-8  
: Sequence 8, Application US/09732350

```

; GENERAL INFORMATION:
;
; APPLICANT: Svendsen, Allan
; APPLICANT: Xu, Feng
;

```

RESULT 8  
US-09-732-350-8  
; Sequence 8, Application US/09732350  
; Patent No. US20010031490A1  
; GENERAL INFORMATION:  
; APPLICANT: Svendsen, Allan  
; APPLICANT: Xu, Peng

QY 273 YDVIEANTPGNWNWTFEGGGLG--GSRNPYPAIFHYAGAP-GGPTDEKAPVD 329  
 Db 266 YSFILTAQDVONMYIRANPBGITTFAGGIN---SALIRDGADVETTTQATSPV- 321  
 QY 330 HNCIDLPLKPVYADVPLSGFAKRAADNTLDVLTGTPLEFKVNGSAINIDMGRAVY 389  
 Db 322 -VLSSESNIAPLTNAAPQLPEVGVGDALNFNLTFFDG-PSLKFQINGV----- 367  
 QY 390 DYVLQNTSPFGYNYV--EVNGADQMS-----YMLIEND-----PGAPFTLPHM 433  
 Db 368 -----TEFPTVVLQILISGASADLLPSGVYALPSNATIELSLPAGALGGPHF 420  
 QY 434 HLHGDFYVIGRSPDESPASNERHVEDPARDAGLLSGANVRVDYSLMPLAFG-WVYLSR 492  
 Db 421 HLHGTFVSV-----RPAQSTTYN-----VAPQVDVYSIGNTGNTIRRD 463  
 QY 493 ADNPGAMLEFHCHIAHVSGGLGVYLERADLR 525  
 Db 464 TNNPGMFLHCHIDMHLLEAALPLSLRTSLTLR 496

## RESULT 10

US-09-732-350-6  
 ; Sequence 6, Application US/09732350  
 ; Patent No. US20010031490A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Svendsen, Allan  
 ; APPLICANT: Xu, Peng  
 ; TITLE OF INVENTION: LACCASE MUTANTS  
 ; NUMBER OF SEQUENCES: 10  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: No. US20010031490A10 No. US20010031490A1disk of No. US20010031490A1th  
 ; STREET: 405 Lexington Avenue  
 ; CITY: New York  
 ; STATE: NY  
 ; COUNTRY: USA  
 ; ZIP: 10174  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Diskette  
 ; COMPUTER: IBM Compatible  
 ; OPERATING SYSTEM: DOS  
 ; SOFTWARE: FastSeq for Windows Version 2.0  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/09/732.350  
 ; FILING DATE:  
 ; CLASSIFICATION:  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: 09/032.315  
 ; FILING DATE:  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Rozek, Carol  
 ; REGISTRATION NUMBER: 36,993  
 ; REFERENCE/DOCKET NUMBER: 5200.200-US  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: 212-867-0123  
 ; TELEFAX: 212-878-9655  
 ; INFORMATION FOR SEQ ID NO: 6:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 599 amino acids  
 ; TYPE: amino acid  
 ; STRANDEDNESS: single  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: protein  
 ; US-09-732-350-6

Query Match 17.2%; Score 542; DB 10; Length 599;

Best Local Similarity 28.6%; Pred. No. 2.5e-38;  
 Matches 168; Conservative 83; Mismatches 218; Indels 118; Gaps 22;

QY 49 PDGVKKEVMVNNISIIPTIFADMGDTIOYVIVNLE---TNGSTIHHGLHOKGRTUL 104  
 Db 35 PDGVTRNAV-LVNGRFPGLITANKGDITKTVRNKLSDPTRRSTTIHMHGLHRTAE 93

QY 105 HDGANGITECPILPPGGRKRVYRFKAQOYSTWYSHFSQAQYNGVYGAIOINGPASTLPY- 163  
 Db 94 EDGPAYVIOCPILPPOESTITYPPLSEQGTWYHSLSQYVDGLGPIVITDPPHD-PYR 152  
 QY 164 -----DTDLGVEPISDYYSADLVELTKNGCAPFSNDVNLNGTAKHPETGEGEYANT 218  
 Db 153 NYVDVDEERTVTLADWYTPSEAL-ATHVDLKITPDGTINGKGY-DPASANTNNT 210  
 QY 219 L-----TPGRHRLILNTSVENHEFOVSLVNHNTMCIIAADMPVNAATVDSLEFLGV 270  
 Db 211 LENLYTLKVRKGRKRYRLIRINASAIASFRRGVQGHCKTIEADGYLTKPIEVDADIDLAG 270  
 QY 271 QRYDVIEANTPGNWNWTFEGGGLGSGSRNPYPAIF-----HAGAP----- 316  
 Db 271 QRYSCILKADQDPDSWINAPITNVL-----NTNVQALLIEDDKRPTTHPMKPLTWKIS 326  
 QY 317 -----GGPPTDEK-----APVDHNCIDLPLKPVYADVPLSG 350  
 Db 327 NEIIQYQWKGHSGHKGKHHKVRALIGVSGLSRVASRSDL-SKRAVELAALAVAG 385  
 QY 351 FA-----KRAADTLDVLTDTGTPLEFKVNGSA-----INIDGRAVVDVLT- QNTS 398  
 Db 386 EAEIDKRONEDNSTYLTETKLIPLVQPCAPGSRADVVPLDGLNPFANGIWTINNVS 445  
 QY 399 FPP-----GYNIYEVNG--ADQMSYMLIEND-----PGAPFTLPHMHLGH 439  
 Db 446 YSPDPVPTLKITLTKDKVDASDTADENTYTLPKNOVVELAIKGAALGIHPLHGH 505  
 QY 440 EYVLGRSPDESPASNERHVEDPARDAGLLSGANPYRVDYSLMPLAFGVLSFRADNPGAM 499  
 Db 506 FDVV-QEGDNAP-----NYNPPRRADVGVGTADG-VAIGRTDMPGW 546  
 QY 500 LEFHCHIAHVSGGLGVYLERADDL-RGAVSPADADDLRLCADMR 545  
 Db 547 FLHCHIDMHLLEGFAMVFAEAPEDIKGSQSVKPPDQMKICEYK 593

## RESULT 11

US-09-944-160-12  
 ; Sequence 12, Application US/09944160  
 ; Patent No. US20020174452A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Lewis, No. US20020174452A1man  
 ; APPLICANT: Davin, Laurence  
 ; APPLICANT: Huang, Ning  
 ; TITLE OF INVENTION: Monocot Seeds with Increased Lignan  
 ; FILE REFERENCE: WSUR117983  
 ; CURRENT APPLICATION NUMBER: US/09/944.160  
 ; CURRENT FILING DATE: 2001-08-30  
 ; PRIOR APPLICATION NUMBER: US 60/230.632  
 ; PRIOR FILING DATE: 2000-09-07  
 ; NUMBER OF SEQ ID NOS: 49  
 ; SOFTWARE: FastSeq for Windows Version 4.0  
 ; SEQ ID NO 12  
 ; LENGTH: 564  
 ; TYPE: PPT  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: Laccase amino acid sequence from plasmid PAP1245  
 ; US-09-944-160-12

Query Match 14.1%; Score 446; DB 9; Length 564;

Best Local Similarity 26.2%; Pred. No. 3.4e-30;  
 Matches 142; Conservative 72; Mismatches 206; Indels 122; Gaps 21;

QY 55 EKVLMVNNISIIPTIFADMGDTIOYVIVNLENTNGSTIHHGLHOKGRTULHDGANGITEC 114  
 Db 46 KSIFVYNGQFPGPTIYATBEGDTIIVDVIINQSEAVT-IHMGVAKQPRPWSGPTITQC 104  
 QY 115 PIPPGGRKRVYRFKAQOYSTWYSHFSQAQYNGVY-GAIOI--NGPASPYPD-DLGVF 170  
 Db 105 PIPGANGFSOKITLSDDELITLWMAH--SDMSRAIVHGAIVIRPNNSNYPRPTDAEAT 162

Db 172 HHAAHITAEANVRCQAGLYMLTDPAEDALNPSGGEEDIMILTSKOTYANGNLVTNN 231  
Qy 188 KNSGAPESDNVLENGTAKHETGEGEYANVTLPGRHRLRLINTSVENHFOVSLVNHNM 247  
Db 232 GELNFWGDIHVHNGQ-----PMPEKVV-----EPKKYFRFLDAAVSRSGLYEADTD- 280  
Qy 248 CIIAAD-WPVNAMTVDS-----LFLVGGRVYVLEANTPGNWFNTYFGGG 295  
Db 291 ---AIDRLRPFKVIASDGLLEHPADTSLITYISMAERYVVDDESDYAK----- 327  
Qy 296 ILGGSRRNPYPAIFHYAGAPGPPTEGKAPVDHNCIDLPLKPYVARDVPLSGFARKA 355  
Db 328 -----TIELNKGSGISGIGTD-----TDYDNTD-KYMRFPVADDTQPDTSVVP 371  
Qy 366 DNTLDVTL-DTGTPLP-----VWKVGSAINIDMGRAVVDVLTQNTSFPFGYNI 405  
Db 372 ANLRVVPSPPTNTPTNPFREFRTGPTWTINGVAF-----ADVQRLLAN----- 416  
Qy 406 VEVNADQMSVYLIENDPCAPFTLPHPHMLHGDFYVLCRSDESPASNERHVPDPARDA 465  
Db 417 VPVGTVERRME-LINAGNG---WTHPHILHVDKVISR---TSGNNAFTVM--PYES 464  
Qy 466 GILSGANPVRDYSMLPAFGVYL-SFRADNPGAMLHCHIAMHYSGGLGVYLERADDL 524  
Db 465 GL-----KDVWLGRRREYVVEAHYAPFPGVYMFCHNLHEDHDMMAAFNATVLPD 516  
Qy 535 RGAVSADADADDLRLCADWRRYPTNPPYKSDSGLKHRRVEGEGELYKA 573  
Db 517 YGYNATVFVDPMEL-----WQARPYE-----LGEFQAQSGQSFVQA 553

RESULT 14  
US-10-080-233-4  
; Sequence 4, Application US/10080233  
; Patent No. US20020151450A1  
; GENERAL INFORMATION:  
; APPLICANT: Wang, Huanling  
; TITLE OF INVENTION: No. US20020151450A1 Phenol Oxidizing Enzymes  
; FILE REFERENCE: GC567  
; CURRENT APPLICATION NUMBER: US/10/080,233  
; CURRENT FILING DATE: 2002-02-19  
; NUMBER OF SEQ ID NOS: 5  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 4  
; LENGTH: 568  
; TYPE: PRT  
; ORGANISM: Bilirubin oxidase  
US-10-080-233-4

Query Match 6.3%; Score 198; DB 12; Length 568;  
Best Local Similarity 22.9%; Pred. No. 4.3e-09;  
Matches 133; Conservative 64; Mismatches 246; Indels 138; Gaps 31;

Qy 23 YEVDSPDTCGVNVPYT-----LTLLEVDMNTGPDGVVKEKVMLVNNSIIIGPTIFADMDCTIQ 78  
Db 77 YEVE-----IKPFTHQVYVPLDGSAD-LVGYDMSR-----GPTFOVPRGVEYV 118  
Qy 79 VTVINNLETNGTSIMHGLHQGTNLHDG-ANGITECPPIPPKGRKYRFRKAQOYGTSMY 137  
Db 119 VAFINNAER-PRSVHLHGFSRAA--FDGWAEDITE--PSGFKOYYVPPNQSAFTLWY 171  
Qy 138 HS--HFSNQYQ-KGVVCAIQINGRA--SLPYDTDLGVPI-----SDIYSSADELVELT 187  
Db 172 HDHAMHITAEANVRCQAGLYMLTDPAEDALNPSGGEEDIMILTSKOTYANGNLVTNN 231  
Qy 188 KNSGAPESDNVLENGTAKHETGEGEYANVTLPGRHRLRLINTSVENHFOVSLVNHNM 247  
Db 232 GELNFWGDIHVHNGQ-----PMPEKVV-----EPKKYFRFLDAAVSRSGLYEADTD- 280  
Qy 248 CIIAAD-WPVNAMTVDS-----LFLVGGRVYVLEANTPGNWFNTYFGGG 295  
Db 281 ---AIDRLRPFKVIASDGLLEHPADTSLITYISMAERYVVDDESDYAK----- 327

Qy 296 ILGGSRRNPYPA--IFHYAGAPGPPTEGKAPVDHNCIDLPLKPYVARDVPLSGFAR 353  
Db 338 IGGIGTDYDITDKYMRFPVADDTQPDTSVPA--NLNEDVFPSPPTNR----- 386  
Qy 354 RADNTLDVTLDTGTPLFWKVGSAINIDMGRAVVDVLTQNTSFPFGYNIYEVGADQ 413  
Db 387 -----QPFEGRTGP---TWTLINGVAF-----ADVQRLLAN-----VPVGTV 422  
Qy 414 WSVYLIENDPGAPFTLPHPHMLHGDFYVLCRSDESPASNERHVPD-PARDAGLLSGAN 472  
Db 423 WE--LINAGNG---WTHPHILHVDKVISR---TSGNNAFTVMPEESKOVYWLIG--- 469  
Qy 473 PYARDYSMLPAFGVYLSRADNPGAMLHCHIAMHYSGGLGVYLERADDLGANSDDAD 532  
Db 470 --RRETV-----VEAHYAPFPGVYMFCHNLHEDHDMMAAFNATVLPDYGNATVP 520  
Qy 533 ADDDLRLCADWRRYPTNPPYKSDSGLKHRRVEGEGELYKA 573  
Db 521 VDPMEEL-----WQARPYE-----LGEFQAQSGQSFVQA 549

RESULT 15  
US-09-338-723A-2  
; Sequence 2, Application US/09338723A  
; Patent No. US20020019038A1  
; GENERAL INFORMATION:  
; APPLICANT: Huaming, Wang  
; TITLE OF INVENTION: Phenol Oxidizing Enzymes  
; FILE REFERENCE: GC561-2  
; CURRENT APPLICATION NUMBER: US/09/338,723A  
; CURRENT FILING DATE: 1999-06-23  
; PRIOR APPLICATION NUMBER: 09/220,871  
; PRIOR FILING DATE: 1998-12-23  
; NUMBER OF SEQ ID NOS: 11  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 2  
; LENGTH: 594  
; TYPE: PRT  
; ORGANISM: Stachybotrys chartarum  
US-09-338-723A-2

Query Match 6.2%; Score 197; DB 10; Length 594;  
Best Local Similarity 24.8%; Pred. No. 5.5e-09;  
Matches 138; Conservative 62; Mismatches 216; Indels 140; Gaps 35;

Qy 33 VREYTLTLEVDMNTGPDGVVKEKVMLVNNSIIIGPTIFADMDCTIQYVTVINNLETNGTSI 92  
Db 107 LRATL-----VGYDMSR-----GPTFNVRGRTETVYRFLNN-ATVENSV 146  
Qy 93 HHGHLHQGTNLHDG-ANGITECPPIPPKGRKYRFR-KAQOYGTSMYHSH-FSQOYGN-- 147  
Db 147 HLGFSRSRAP--FDGWAEDVT--FP--GEYKDYFPFNQOSARLLWHDHAFKTAENAY 199  
Qy 148 -GVVCAIQINGRA--SLPYDTDLGVPI-----SDIYSSADELVELTKSGAPESDNV 199  
Db 200 FQAGAYIITNDEKDALGLPSCYGEEDIPILITAKTI--NADGTINSTEG--EDDL 252  
Qy 200 FNGTAKHETGEGEYANVTLPGRHRLRLINTSVENHFOVSLVNHNM-----MCIIAA 252  
Db 253 W-GDVIHVHNGQPPPLNV--QPRKRYFRFLNAVASAMLLIYLRSSPVVRILPQVIAS 308  
Qy 253 DMYFVVA-WTVDSLFLVGGRVYVLEANTPGNY--WPNVTGGGGLCGGSRNPYPAA- 308  
Db 309 DAGLLDAPVOTSNLYLAVERYEIIIDFTNFAQOTDLRNVAAFTNDV--GDEDEVARTL 365  
Qy 309 -IFHYAGAPGPPTEGKAPVDHNCIDLPLKPYVARDVPLSGFARKADNTLDTLDTTG 367  
Db 366 EWRKFEVSSG--TVEDNSQV-----DSTLDVDP--PPPKKEPADHHEKFE- 407  
Qy 368 TPLEVWKVGSAINIDMGRAVVDVLTQNTSFPFGYNIYEVNAGDQMSYMLIENDPGAP 427  
Db 408 -----RSNGHYLINDVGFADV--ERVLAPRELGTVEV-----WELENSSGG-- 447

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OM protein - protein search, using sw model

Run on: December 4, 2002, 10:43:44 ; Search time 22 Seconds

(without alignments)  
2503.865 Million cell updates/sec

Title: US-09-869-877-10

Perfect score: 3158  
Sequence: 1 QOQSCNTPSNRACWTDGTDIN.....KSDSGIKHRWVEGEMLVKA 573

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database : 1: p1r1:\*  
2: p1r2:\*  
3: p1r3:\*  
4: p1r4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2231.5	70.7	621	2 S72493	laccase (EC 1.10.3
2	2032	64.3	619	1 KSNCLD	laccase (EC 1.10.3
3	2021	64.0	619	1 KSNCLT	laccase (EC 1.10.3
4	616	19.5	520	2 B35883	ligninolytic pheno
5	615	19.5	520	2 A35883	laccase (EC 1.10.3
6	612.5	19.4	529	2 S68120	laccase (EC 1.10.3
7	603	19.1	520	2 JCS356	laccase (EC 1.10.3
8	602	19.1	520	2 S53533	laccase (EC 1.10.3
9	583.5	18.5	527	2 JCS357	laccase (EC 1.10.3
10	573	18.1	512	2 JCS355	laccase (EC 1.10.3
11	568	18.0	624	2 A36962	laccase (EC 1.10.3
12	565	17.9	572	2 S68119	laccase (EC 1.10.3
13	558	17.7	576	2 S68117	laccase (EC 1.10.3
14	556	17.6	548	2 S18746	laccase (EC 1.10.3
15	547.5	17.3	582	2 T05020	l-ascorbate oxidas
16	542	17.2	599	2 S68118	laccase (EC 1.10.3
17	541.5	17.1	529	2 S49120	laccase (EC 1.10.3
18	531.5	16.8	533	2 S63371	laccase (EC 1.10.3
19	526.5	16.7	622	2 S62580	probable multicop
20	499.5	15.8	622	2 S66353	l-ascorbate oxidas
21	495.5	15.7	21	2 S56214	probable membrane
22	490	15.5	567	2 T44928	l-ascorbate oxidas
23	488	15.5	557	2 JCS229	l-ascorbate oxidas
24	483.5	15.3	636	2 A55428	ferroxidase precu
25	475	15.0	587	1 KSKVAO	l-ascorbate oxidas
26	470.5	14.9	579	2 S11027	l-ascorbate oxidas
27	463.5	14.7	552	2 A51027	l-ascorbate oxidas
28	456.5	14.5	553	2 T45959	laccase-like prote
29	453	14.3	573	2 T02743	laccase (EC 1.10.3

#### ALIGNMENTS

30	450	14.2	586	2 T45945	laccase-like prote
31	448.5	14.2	569	2 T48484	laccase-like prote
32	448.5	14.2	520	2 T00579	probable laccase
33	442.5	14.0	580	2 T48488	probable laccase
34	442.5	14.0	584	2 T45944	probable laccase
35	442	14.0	551	2 T02752	probable laccase
36	438	13.9	554	2 T01240	laccase (EC 1.10.3
37	434.5	13.8	555	2 T48347	laccase-like prote
38	415	13.1	576	2 E86316	protein T10022.11
39	411.5	13.0	569	2 E84904	probable laccase
40	362	11.5	609	1 KSA5L1	laccase (EC 1.10.3
41	361	11.4	713	2 T21201	hypothetical prote
42	344	10.9	632	2 F83387	copper resistance
43	340.5	10.8	504	2 F70813	hypothetical prote
44	333.5	10.6	611	2 C82845	copper resistance
45	332.5	10.5	605	2 S52253	copper resistance

RESULT 1  
S72493  
laccase (EC 1.10.3.2) precursor - Podospora anserina  
N:Alternate names: benzenediol:oxigen oxidoreductase; urishiol oxidase  
C:Species: Podospora anserina  
C:Date: 24-Oct-1998 #sequence\_revision 24-Oct-1998 #text\_change 21-Jul-2000  
C:Accession: S72493  
R:Fernandez-Larrea, J.; Stahl, U.  
Mol. Gen. Genet. 252, 539-551, 1996  
A:Title: Isolation and characterization of a laccase gene from Podospora anserina.  
A:Reference number: S72493; MIMD:97071669; PMID:8914515  
A:Molecule type: DNA  
A:Residues: 1-621 <PER>  
A:Cross-references: EMBL:Y08827; NID:q1729780; PIDN:CAA70061.1; PID:q1729781  
A:Experimental source: strain ATCC 26003  
C:Genetics:  
A:Gene: lac2  
A:Insertions: 80/3; 111/1; 134/2  
C:Function:  
A:Description: catalyzes one-electron oxidation of mono-, di- and polyphenols, amin  
C:Superfamily: laccase  
C:Keywords: copper; glycoprotein; oxidoreductase  
F:1-23/Domain: signal sequence #status predicted <SIG>  
F:24-48/Domain: amino-terminal propeptide #status predicted <PRO>  
F:49-605/Product: laccase #status predicted <CAT>  
F:74-209/Domain: amino-terminal beta-barrel #status predicted <BB1>  
F:210-366/Domain: middle beta-barrel #status predicted <BB2>  
F:431-528/Domain: carboxyl-terminal beta-barrel #status predicted <BB3>  
F:606-621/Domain: carboxyl-terminal propeptide #status predicted <CTP>  
F:133,261,276,289,325,334,382,401,421,441/Binding site: carboxylate (Asn) (covalent  
F:138,479/Binding site: copper (His) (type 2) #status predicted  
F:140,183,185,481,548,550/Binding site: 2Cu-O cluster (His) (copper type 3) #status  
F:476,549,554/Binding site: copper (His, Cys, His) (type 1) #status predicted

Query Match 70.7%; Score 2231.5; DB 2; Length 621;  
Best Local Similarity 68.9%; Pred. No. 7.8e-156;  
Matches 397; Conservative 65; Mismatches 109; Indels 5; Gaps 4;

QY	1	QOQSCNTPSNRACWTDGTDINDEYDSDPGVVRPYTLTTEVDNMGPPGVKEMLV	60
DB	46	QSSCHTANRCAVPGDINTDEYSPNNGVTRTYTLTTEVDNMGPPGVAKQKMLV	105
QY	61	NNSIIGPTIFADMGDTIQVTVNNLTETNGTSHHGHGKGTNLHDGANGITECPPIPKG	120
DB	106	NGDIFGPTITANMGDWIQVAVNNLTETNGTSHHGHGKGTNNHDGANGTECPPIPKG	165
QY	121	GKYYRFAKQYQYGTSTHSHFSAYQYGVGAIQINGPASPILPTDLCVPPISDYYS	180
DB	166	GSRIYRFAKQYQYGTSTHSHFSAYQYGVGAIQINGPASPILPTDLCVPPISDYYS	225
QY	181	DELVELKNGSGAPRSDVNLNGTAKHPEVTEGGEYANTLTLPGRHRRLRLNTSVENHFOV	240



[illegible][illegible]

```

RESULT 5
A35883
laccase (EC 1.10.3.2) A - white-rot fungus (Trametes versicolor)
NAlternate names: ligninolytic phenoloxidase I precursor
C:Species: Trametes versicolor (white-rot fungus)
C:date: 23-Oct-1990 #sequence_revision 23-Oct-1990 #text_change 19-May-2000
C:Accession: A35883; S59526
R:Kojima, Y.; Tsukuda, Y.; Kawai, Y.; Tsukamoto, A.; Sugiyura, J.; Sakano, M.; Kita,
J. Biol. Chem. 265, 15224-15230, 1990
A>Title: Cloning, sequence analysis, and expression of ligninolytic phenoloxidase ge
A:Reference number: A35883; PMID:2394718
A:Accession: A35883
A>Status: preliminary; not compared with conceptual translation
A:Molecule type: DNA
A:Residues: 1-520 <KOJ>
A:Cross-references: GB:M60560; GB:J05562; NID:g167464; PIDN:AAA33103.1; PID:g167465
R:Joerensen, L.; Sjoestrom, K.; Haegstroem, I.; Nyman, P.O.
Biochim. Biophys. Acta 1251, 210-215, 1995
A>Title: Characterization of a laccase gene from the white-rot fungus Trametes versi
A:Reference number: S59526; PMID:95399443; PMID:7669813
A:Accession: S59526
A>Status: preliminary
A:Molecule type: protein
A:Residues: 351-360 <JOE>
C:Superfamily: laccase
C:Keywords: oxidoreductase

Query Match          19.5%; Score 615; DB 2; Length 520;
Best Local Similarity 31.6%; Pred. No. 2, 6e-37;
Matches 173; Conservative 73; Mismatches 212; Indels 90; Gaps 21;

QY      37 TLTLEFVDMWTGGDGVKKERMLVNNSITGPTFFADMGPTIOVTVINLNTLN-----GTSI 92
       | | | : | | | : | | | | | : | | : | | : | | | | | | | | |
DB      26 TADLTISNAEVSPEDGARARAV--VNNVTPGPPLVAGKGKGRFOALNVIDLNLTHRLMASTSI 84

QY      93 HHWGHLQKQTNLDHGANGITECEPIPPKRGKRKYVRFA--QOYGTSWYSHSFSAOYGNGVG 151
       ||| |||| | | : ||| | : ||| | | |||| | | : | |
DB      85 HWHGFQFKTNNMADGAFAFNQCPI--SSGHSFLDFQVPDQAGTFWYHSHLSHCGLRG 143

QY      152 ALQI---NKPASLPPTYDLG--VFPSDYIYSAADELVELTKRSGAPF---SNVNFENGT 203
       : | | : | | | | : | | : | | : | | : | | : | | : | | |

```



```

Db      137 QYCGDLGPMWVYVPSD - PHADLYDVODETTIITLSDMWHTAA-----SIGAAPIG 187
QY      195 SDANLFLNGCIAKHPTGSGGEFANATLPGRNHRRLINTSYENHFOVSLYVHTMCTIADM 254
Db      188 SDSTLLINGLRFPAGSDSTDLAVTTVEBQKRYRRRLSLSCDPNYVYSIGHMNTIIEEDA 247
QY      255 VPVAAKTVDSLEFVGQRYVYVEANRTPCNTMYF-----NTFPGGGLGGSSNPYA 307
Db      248 VNHREPLVDSIQIYAGGRYSFVLTAQDDIDNTIRALPSAGTTSSEFGGI-----NS 298
QY      308 AIFHYACAGCGPPTDEGKADVDHNCIDLPLKAEVVARVDYLSGFAKRAKDNTLDVLTDTG 367
Db      299 AILKYSGASEVDPTTETTSV--LPIDEAIVLYDSPAAGDPNIGVDYALNDLPNFG 356
QY      368 TPLEPMKVNVSAINIDMGRAVDVYLTQNTS-----PPG-YAIVEVNGADQMSYUL-IEH 421
Db      357 TNEFIIDSVSVSPV-----PVLLQILISGTTSAADLLPSGLPRAVPSNSTIEFPIATYN 412
QY      422 DPGAFETLPFPHMLHGHEDFYVLRSPDESPASNERHVPADAGL--LSGANPRAVRS 479
Db      413 APGA-----PPRFLHGHTEFSY-----RTAGSTDNFNPVPRRDVY 449
QY      480 MLPAFG-VWVLSFRADPGAMLFHCIIAMHVSGLGAVVLEBADDLKGAVSDADADDLR 538
Db      450 NTGVGVDNVTIRFTTDPNPGWFLHCIDHLEAGFAIVSEDTADVSNTTPTSTA----- 504
QY      539 ICADMIKRYPT-NPYKSD 556
Db      505 ----WEDLCPTYNALDSSD 519

```

## RESULT 8

I:Accession: 559533  
 A:Reference number: 559526; MUID:9539443; PMID:7669813  
 A:Cross-references: EMBL:X84683; NID:9886718; PIDN:CAA59161.1; PID:9886719  
 A:Residues: 1-520 <JOE>  
 A:Molecule type: DNA  
 C:Keywords: oxido-reductase  
 F:1-32/Domain: signal sequence #status predicted <MA>  
 F:32-350/Product: laccase #status predicted <MA>  
 C:Superfamily: laccase  
 A:Intfons: 62/3; 85/3; 126/1; 185/2; 217/2; 269/3; 335/3; 424/3; 463/3; 503/1  
 C:Species: Trametes versicolor (white-rot fungus)  
 C:Date: 20-Jul-1996 #sequence\_revision 08-Nov-1996 #text\_change 19-May-2000  
 C:Accession: 559533  
 R:Jensson, L.; Stenstrom, K.; Haegstroem, I.; Nyman, P.O.  
 Biochim. Biophys. Acta 1251: 210-215, 1995  
 A:Title: Characterization of a laccase gene from the white-rot fungus Trametes versicolor

Query Match	19.1%	Pred. No. 602;	DB 2;	Length 520;
Best Local Similarity	32.0%	Pred. No. 2.3e-36;		
Matches 179;	Conservative 77;	Mismatches 211;	Indels 92;	Gaps 24

[illegible]

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Db      248 VNHBEPLAVDSIQIYAAGRYSFVLZLADDDIDNFIKALPSAGTTSFPGCI-----NS 298
QY      308 AIFHYACAPGPPPLDECKAPYDHNKCLDLPMUKPYVAVADVLSGFAKRAADLTLDVTLDTTG 367
Db      299 AILRYSQASEVDPPTTETTSV--LPIDEANILVPLDSPAAGDDNIGVDVALMIDNENFDC 356
QY      368 TPLEVMKNGCSAINIDWGRAVADVLTQMS----PPGQ-YNIVEVNGADQMSYWL-IEH 421
Db      357 TNEFINOVSPSPVY-----FVLQILSGTTSADLLEPGLFALPSNSTIEISFPIATN 412
QY      422 DPGAPFTLLPHEMHLGHDFYVLGRSPDESPASNERHYVDPADAGL--ISGANPVARDVS 479
Db      413 APGA-----PHEFHLLGHFTSIV-----FRAGSDTNEFVNPVRDYY 449
QY      480 MLRPFQ--WVVLSPFADNPQAMLFHCHTAMVSGGLGVYTLERADDLKGAVSDADDLDR 538
Db      450 NTGTAGGNVYIRFTDNDPBGWFLCHIDHLEAGFAIVSEJEDADVSNNTTTPSTA----- 504
QY      539 LCADMRRTWPT-NPYPKSD 556
Db      505 ----WEDLCPTYNALBSSD 519

```

## RESULT 9

A:Enzyme: EC 1.0.3.2) 5 precursor - white-rot fungus (Trametes villosa)  
N:Alternate names: urushiol oxidase  
C:Species: Trametes villosa (white-rot basidiomycete)  
C:Date: 28-May-1997 #sequence\_revision 18-Jul-1997 #text\_change 19-May-2000  
C:Accession: J05357  
R:Yaver, D.S.; Golightly, E.J.  
Gene 181, 95-102, 1996  
A:Title: Cloning and characterization of three laccase genes from the white-rot basidiomycete *Trametes villosa*  
A:Reference number: J05355; M01D:97128774; PMID:8973314  
A:Accession: J05357  
A:Molecule type: DNA  
A:Residues: 1-527 <YAV>  
A:Cross-references: GB:L78078  
C:Comment: This enzyme is a multi-copper enzyme which catalyzes the oxidation of phenolic compounds.  
C:Genetics:  
A:Gene: lcc5  
A:Strains: 63/3; 86/3; 127/1; 165/1; 186/2; 220/2; 272/3; 357/3; 431/3; 470/3; 509/3  
C:Superfamily: laccase  
C:Keywords: oxidoreductase  
F:1-23/Domain: signal sequence #status predicted <SIG>  
F:24-527/Product: laccase 5 #status predicted <NAV>

Query Match	18.5%;	Score 583.5;	DB 2;	Length 527;
Best Local Similarity	30.5%;	Pred. No. 5.5e-35;		
Matches 178;	Conservative 66;	Mismatches 202;	Indels 137;	Gaps 26

```

QY 31 GVAPEPY-LTLEVDNMTGQGVYKKEVLAUNNSIIETPIADMGDTIQYTVINN--ET 87
      | : | | : | | : | | : | : | : | : | : | : | : | : | : | : |
Db 23 GAIPETDITLISNAD--VTPDGITRAAV-LAGGVPEPPLITGNKGDFQINVIDIINET 79
      | : | | : | | : | | : | : | : | : | : | : | : | : | : | : |
QY 88 --NCTSIHMHGILHDKGTNLHNGANGIRECEPIPKGGRKRYRFKA-QQYGTSMYHSFSAQ 144
      | : | : | : | | | : | : | : | : | : | : | : | : | : | : | : |
Db 80 MLKSTTIIHMHGIFQAGTNMADGAFAVNWQCP-ATGNSFLDFTVPDQAGFFWHSHLSIQ 138
      | : | : | : | | | : | : | : | : | : | : | : | : | : | : | : |
QY 145 YGNCVGAIAQINCP----ASL-PRDTDLGVFPISDIYYSSADELVELTKNSGAF---SD 166
      | : | : | : | : | : | | | | | : | : | : | : | : | : | : | : |
Db 139 YCDLSRPLVLVYDDPDNPASLIDVDDDTVTYITLADWYHTAA-----KIGFPPAGPD 190
      | : | : | : | : | : | | | | | : | : | : | : | : | : | : | : |
QY 197 NVLENTAKAPETGEG--EYANVTLLPGRKRIILLMTSYENHFOVSLVNHKTIADAM 254
      | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 191 SYLLNGRGRESGDOGGAINTLVITVQGRKYRFRFLVATISCDPMTFSIDGNHTIIEVDS 250
      | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
QY 255 VPVNAKMYDLSLGLVQGRDYVTEAKNTPEKNTPENV-----TRGGGLCCGSRKPYP 306
      | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 251 VNHEDLVDSIQIPAGGRYSFLNANSDIDNWTIRALPNTGTDTDTGG-----VN 300

```

DB 492 ICRGGAISINDLITNI-DETLID-----NPKKDTLWIOGSSWAVLRTITADPGWALH 543  
QY 503 CHIAHVS-GGLGVYLERADDLRGAVSDADA-DDLDRICAD 542  
DB 544 CHIGHMTEKGLAVIVQPS-----AIGHMESPESTNINCAN 580

## RESULT 12

568119  
laccase (EC 1.10.3.2) 3 precursor - Rhizoctonia solani  
C:Species: Rhizoctonia solani  
C:Date: 19-Mar-1997 #sequence\_revision 19-Mar-1997 #text\_change 20-Jun-2000  
C:Accession: S68119  
R:Wahlthier, J.A.; Xu, F.; Brown, K.M.; Brown, S.H.; Golightly, E.J.; Halkier, T.; Kaur, Genet. 29, 395-403, 1996  
A:Title: The identification and characterization of four laccases from the plant pathogen  
A:Reference number: S68117; MUID:96171523; PMID:8598061  
A:Accession: S68119  
A:Status: nucleic acid sequence not shown  
A:Molecule type: DNA  
A:Residues: 1-572 <MAH>  
A:Cross-references: EMBL:Z54215; NID:G1150565; PIDN:CAA90942.1; PID:G1150566  
A:Experimental source: strain RS22  
C:Genetics:  
A:Gene: lcc3  
A:Introns: 45/1; 81/3; 102/3; 145/1; 146/1; 186/2; 273/3; 380/3; 404/3; 441/2; 476/3; 52  
C:Superfamily: laccase  
C:Keywords: copper; oxidoreductase  
F:1-19/Domains: signal sequence #status predicted <SIG>  
F:19-572/Product: laccase 3 #status predicted <MAT>

Query Match 17.9%; Score 565; DB 2; Length 572;  
Best Local Similarity 31.2%; Pred. No. 1.4e-33;  
Matches 176; Conservative 60; Mismatches 206; Indels 122; Gaps 22;

QY 49 PDGVKENVKVMVNNISITPTIFADMGDTQVYVNNLEFN-----GTSIHMHGILH 103  
DB 35 PDGVKRD-ATLVNGYRGGLTIFANKGDTLKVONKL-TNPMYRTTSIHMHGILH 92  
QY 104 LHDGANGITECPPIPKKGKRYRFRKAQYGTSMYSHSFAQYGVGAIOINGPASLPY 163  
DB 93 DDDGAFVYQCIYVQASTYTMPLGDDGTGYWYHSHLSQYVGLRGVLVYDKRD-PH 151  
QY 164 -----DTDLGVFPISDYIYSSADELVELTKNSGAPFSDNVLENG-----TAKHPT 209  
DB 152 RRLYDIDDEKTVLILIGDWYHSSKAIL-ATGNITLQOPDSATINCKGRPDONTFANPMT 210  
QY 210 GEGEANTLTTPGRHRLRLINTSVENHFOVSLVNHMTKIIADAVPVNAKTVDSLELGV 269  
DB 211 -----LYTLKVRKGRKRYRLKVINSSAIFRMSIOGHKMTVIAADVSTKPYGVDSFDILA 266  
QY 270 GORYDVLEANTPGNYFNV-----TFGGGLCGGSRNPY-----PAI 309  
DB 267 GORIDAVVEANDEPTTYMINAPLVANKTAQALLIEDRRPYRPRKPYRKMSVSEAI 326  
QY 310 FHYAGAPGPTDEG-----KAVDHNCLDLPNLKPVVARD-----VPLS--G 350  
DB 327 IKYWHKRGRLSGHGLKAMMEGSLHIGRDIYKQNETTYVMDETKLVPLEHFG 386  
QY 351 FA-----KRADNTLDVTLD---TTGTPLFWKVG-----SAINIIDGRAVVOYV 392  
DB 387 AACGSKPADLVLDLTFGVNFTTGH---WMINGIPHKSPDMPTLKITLDTDGVTESDPT 442  
QY 393 LTQNTSPFGYIVVEVNGADQSWYLIENTDPAPFTLPHMLHGHDFVL--GRSPDES 450  
DB 443 QPEHTLILPKKNCVFEN-----IKGNSG--LGIYHPIHLHGHTEPVVQFGNNP-- 489  
QY 451 PASNERHVPDPAAGLISGANPVRRDYSMCLPAFGVNVLSFRADNGAMLFCHCHIAHVS 510  
DB 490 -----NYVNPRRDYVGATDEG--VRFQFTDNDPWFGLCHIDHWLE 530  
QY 511 GGLGVYLERADDLRGAVSDADAD 534

DB 531 EGFAMVFAEAPPAIKGPKSPVD.554

## RESULT 13

568117  
laccase (EC 1.10.3.2) 1 precursor - Rhizoctonia solani  
C:Species: Rhizoctonia solani  
C:Date: 19-Mar-1997 #sequence\_revision 19-Mar-1997 #text\_change 13-Mar-1998  
C:Accession: S68117  
R:Wahlthier, J.A.; Xu, F.; Brown, K.M.; Brown, S.H.; Golightly, E.J.; Halkier, T.; Kaur, Genet. 29, 395-403, 1996  
A:Title: The identification and characterization of four laccases from the plant pathogen  
A:Reference number: S68117; MUID:96171523; PMID:8598061  
A:Accession: S68117  
A:Status: nucleic acid sequence not shown  
A:Molecule type: DNA  
A:Residues: 1-576 <MAH>  
A:Cross-references: EMBL:Z54275  
A:Experimental source: strain RS22  
C:Genetics:  
A:Gene: lcc1  
A:Introns: 45/1; 81/3; 102/3; 145/1; 146/1; 186/2; 273/3; 381/3; 405/3; 442/2; 477/3  
C:Superfamily: laccase  
C:Keywords: copper; oxidoreductase  
F:1-19/Domains: signal sequence #status predicted <SIG>  
F:20-576/Product: laccase 1 #status predicted <MAT>

Query Match 17.7%; Score 558; DB 2; Length 576;  
Best Local Similarity 30.6%; Pred. No. 4.6e-33;  
Matches 182; Conservative 63; Mismatches 212; Indels 138; Gaps 28;

QY 44 DMTGPDGVKENVKVMVNNISITPTIFADMGDTQVYVNNLEFN-----GTSIHMHGILH 98  
DB 30 DGEIAPDG-VKRNATLVNGYRGGLTIFANKGDTLKVONKL-TNPMYRTTSIHMHGILH 87  
QY 99 QKGTMLHOGANGITECPPIPKKGKRYRFRKA---QOYGTSMYSHSFAQYGVGAIOI 155  
DB 88 QHRNADDDGSPSTVCCPIYV---RESYTYTTPLDODGTGYWYHSHLSQYVGLRGPLVI 144  
QY 156 NGPASLPY-----DTDLGVFPISDYIYSSADEL-----VELTKNSGAPFS-DN 197  
DB 145 YPKRD-PHRLYDVDEKTVLILIGDWYHSSKAILASGTTORRVSATINCKGRPDNP 203  
QY 198 VLENGTAKHPTGEGEYANVTLTPGRHRLRLINTSVENHFOVSLVNHMTKIIADAVPV 257  
DB 204 -----TPANPD-----LYTLKVRKGRKRYRLKVINSSAIFRMSIOGHKMTVIAADVST 254  
QY 258 NAMTVDSLEFLVGQRYDVYIEANRTPGNYFNV-----TFGGGLCGGSRNPY----- 305  
DB 255 KPYQVADADILAGORIDCIVEANDEPTTYMINAPLVANKTAQALLYEDRRPYRPRK 314  
QY 306 -----PAIFHY-----AGAPGAPPTD--EGKAPV-DHNCILDLPNLKPVYA 343  
DB 315 GYRKMSVSEAITIKYWHKRGRLSGHGLKAMMEGSLHIGRDIYKQNETTYV 374  
QY 344 RD-----VPLS--GFA---KRADNTLDVTLD---TTGTPLFWKVG-----SA 379  
DB 375 MDESKLVPLEYGAAGSKPADLVLDLTFGLNFATGH---WMINGIPESKPIPLKI 430  
QY 380 IINIDGRAVVOYVLTQNTSPFGYIVVEVNGADQSWYLIENTDPAPFTLPHMLHGH- 438  
DB 431 LTDEGVYESDPTKEHNYVILPKKNCIEN-----IKGNSGIPIT--HVIHLHGT 479  
QY 439 -DFYVIGSPDESPPASNERHVPDPAAGLISGANPVRRDYSMCLPAFGVNVLSFRADNG 497  
DB 480 MDVYVQFGNNP-----NYVNPRRDYVGATDEG--VRFQFTDNDPWFGLCHIDHWLE 518  
QY 498 AMLFCHCHIAHVSGLGVYLERADDLRGAVSDADAD-DLDRICADWRRYPTNP 551  
DB 519 PWFGLCHIDHWLEEGFAMVFAEAPPAIKGPKSPVD.573

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OM protein - protein search, using sw model

Run on: December 4, 2002, 10:03:34 ; Search time 14 Seconds

(without alignments)  
1697.567 Million cell updates/sec

Title: US-09-869-877-10

Perfect score: 3158  
Sequence: 1 QOQCNTPSNRACWTGTDGIN.....KSDGLKRWVEGEMLVKA 573

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : SwissProt\_40:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match Length	ID	Description
1	2231.5	70.7	621 1	LAC2_PODAN
2	2032	64.3	619 1	LAC1_NEUCR
3	2021	64.0	619 1	LAC2_NEUCR
4	1849	58.5	591 1	LAC1_CRYPA
5	824.5	26.1	486 1	LAC1_BOTCI
6	636	20.1	520 1	LAC1_TRAVI
7	615	19.5	520 1	LAC1_CORHI
8	603	19.1	520 1	LAC4_TRAVI
9	602	19.1	520 1	LAC4_TRAVE
10	583.5	18.5	527 1	LAC5_TRAVI
11	580.5	18.4	527 1	LAC5_TRAVE
12	571	18.1	519 1	LAC2_TRAVI
13	570	18.0	519 1	LAC2_TRAVE
14	565	17.9	572 1	LAC3_THACU
15	564	17.9	531 1	LAC4_THACU
16	558	17.7	576 1	LAC1_THACU
17	556	17.6	548 1	LAC1_PHLRA
18	546.5	17.3	520 1	LAC2_AGABI
19	541.5	17.1	529 1	LAC1_PLEOS
20	541	17.1	599 1	LAC2_THACU
21	531.5	16.8	520 1	LAC1_AGABI
22	531.5	16.8	533 1	LAC2_PLEOS
23	526.5	16.7	622 1	YAB8_SCHPO
24	510.5	16.2	473 1	LAC3_TRAVI
25	499.5	15.8	578 1	ASO_TOBAC
26	495.5	15.7	622 1	FER5_YEAST
27	483.5	15.3	636 1	FER5_YEAST
28	475	15.0	587 1	ASO_CUCSA
29	474.5	15.0	579 1	ASO_CUCMA
30	472.5	15.0	624 1	ASO_CUCMA
31	463.5	14.7	552 1	ASO_CUCPM
32	362	11.5	609 1	LAC1_EMENT
33	332.5	10.5	605 1	PCOA_BCOLI

34	328.5	10.4	608 1	YD56_YEAST	Q04399 saccharomyc
35	319	10.1	609 1	COPA_PSESM	P12374 pseudomonas
36	254.5	8.1	554 1	NTF3_TOBAC	P29162 nicotiana t
37	252	8.0	516 1	CUEO_ECOS7	O8K447 escherichia
38	249.5	7.9	555 1	ASO_BRANA	O00624 brassica na
39	249	7.9	516 1	CUEO_ECOS7	P36649 escherichia
40	230	7.3	536 1	CUEO_SALTI	O82961 salmonella
41	228	7.2	536 1	CUEO_SALTY	O82962 salmonella
42	227	7.2	513 1	CORA_BACSU	P07788 bacillus su
43	204	6.5	572 1	BLRO_MYRVE	O12737 myrothecium
44	200	6.3	533 1	CUEO_YERPE	O82bk0.yersinia pe
45	162	5.1	642 1	PHSA_STRAT	Q03692 streptomyc

## ALIGNMENTS

RESULT 1  
LAC2\_PODAN  
ID LAC2\_PODAN STANDARD: PRT: 621 AA.  
AC P78722;  
DT 01-NOV-1997 (Rel. 35, Created)  
DT 01-NOV-1997 (Rel. 35, Last sequence update)  
DT 01-NOV-1997 (Rel. 35, Last annotation update)  
DE Laccase II precursor (EC 1.10.3.2) (benzenediol:oxygen oxidoreductase)  
DE (laccase II precursor) (diphenol oxidase) (laccase C).  
GN LAC2.  
OS Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;  
OC Sordariales; Lasiosphaeriales; Podospora.  
OX NCBI\_TaxID=5145;  
RN (1)  
RP SEQUENCE FROM N.A.  
RC STRAIN=ATCC 26003;  
RX MEDLINE=97071669; PubMed=8914515;  
RA Fernandez-Larrea J., Stahl U.;  
RT \*Isolation and characterization of a laccase gene from Podospora  
RT anserina\*.  
RT Mol. Gen. Genet. 252:539-551(1996).  
RL  
CC -1- FUNCTION: PROBABLY INVOLVED IN LIGNIN DEGRADATION AND IN THE  
CC DETOXIFICATION OF LIGNIN-DERIVED PRODUCTS IN ITS NATURAL HABITAT  
CC (HERBIVOROUS DUNG), WHICH IS RICH IN LIGNIN OF GRASSES AND STRAW.  
CC PROBABLY INVOLVED IN MELANIN SYNTHESIS AND IN PERTHECIA  
CC DEVELOPMENT.  
CC -1- CATALYTIC ACTIVITY: 4 benzenediol + O(2) -> 4 benzoemiquinone + 2  
CC H(2)O.  
CC -1- COFACTOR: BINDS 4 CU-IONS PER MOLECULE. THREE DISTINCT CU  
CC CENTERS KNOWN AS TYPE 1 OR BLUE, TYPE 2 OR NORMAL, AND TYPE  
CC 3 OR COUPLED BINUCLEAR (BY SIMILARITY).  
CC -1- SUBUNIT: MONOMER.  
CC -1- SUBCELLULAR LOCATION: Secreted.  
CC -1- DEVELOPMENTAL STAGE: LOW BASIC LEVELS THROUGHOUT THE GROWTH PHASE;  
CC INCREASES AT LEAST 20-FOLD AT THE BEGINNING OF THE AUTOLYTIC PHASE  
CC AND DECREASES AGAIN THEREAFTER.  
CC -1- INDUCTION: UNDER OXIDATIVE STRESS ON THE MYCELIUM BY AROMATIC  
CC XENOBIOTICS (GUARACOL, HYDROQUINONE, BENZOQUINONE), AND BY COPPER  
CC SALT AT A CONCENTRATION OF 1mM (GROWING MYCELIUM).  
CC -1- PTM: LACCASE II IS PROCESSED AT BOTH ITS N-TERMINUS AND ITS C-  
CC TERMINUS.  
CC -1- MISCELLANEOUS: PODOSPORA ANSERINA CONTAINS AT LEAST 3 LACCASE  
CC ISOFORMS NAMED I, II, AND III. THEY DIFFER IN THEIR SUBSTRATE  
CC SPECIFICITY, NUMBER OF SUBUNITS, ISOELECTRIC POINT AND HEAT  
CC STABILITY.  
CC -1- SIMILARITY: BELONGS TO THE FAMILY OF MULTICOPPER OXIDASES.  
CC -1- SIMILARITY: CONTAINS 3 PLASTOCYANIN-LIKE DOMAINS.  
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FT PROPER 607 619 PLASTOCYANIN-LIKE 1.  
 FT DOMAIN 84 207 PLASTOCYANIN-LIKE 2.  
 FT DOMAIN 216 373 PLASTOCYANIN-LIKE 3.  
 FT DOMAIN 431 566 PLASTOCYANIN-LIKE 3.  
 FT METAL 144 144 COPPER (TYPE 2) (PROBABLE).  
 FT METAL 146 146 COPPER (TYPE 3) (PROBABLE).  
 FT METAL 189 189 COPPER (TYPE 3) (PROBABLE).  
 FT METAL 191 191 COPPER (TYPE 3) (PROBABLE).  
 FT METAL 477 477 COPPER (TYPE 1) (PROBABLE).  
 FT METAL 480 480 COPPER (TYPE 2) (PROBABLE).  
 FT METAL 482 482 COPPER (TYPE 3) (PROBABLE).  
 FT METAL 548 548 COPPER (TYPE 3) (PROBABLE).  
 FT METAL 549 549 COPPER (TYPE 1) (PROBABLE).  
 FT METAL 550 550 COPPER (TYPE 3) (PROBABLE).  
 FT METAL 554 554 COPPER (TYPE 1) (PROBABLE).  
 FT METAL 559 559 COPPER (TYPE 1) (PROBABLE).  
 FT CARBOHYD 139 139 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 282 282 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 295 295 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 340 340 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 422 422 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 444 444 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 SQ SEQUENCE 619 AA; 68198 MW; FDEDD678B65048E3 CRC64;

Query Match 64.3%; Score 2032; DB 1; Length 619;

Best Local Similarity 64.3%; Pred. No. 3.3e-137; Matches 359; Conservative 80; Mismatches 113; Indels 6; Gaps 2;

QY 4 CPTPENRACWMTGVDYNDYEDVSDPTGVVPRYTLLTFEVDWMTGPDGVKRYKLVNNS 63  
 DB 55 CNSPFRNROCHSGFENINDYELGTENTGKTKRKLITETDWMIGPDVYIKKVMVNDK 114  
 QY 64 IIGPTIFADWGTIOVTVYNNETNGSTIHWGLHOKGTNLHDGANGITECPDIPKGRK 123  
 DB 115 IIGPTIADWGYIEITVINKLKSNGSTIHWGHMQRNINODGVNGVTECPDIPKGRK 174  
 QY 124 VYRFRAGQYGTSMYSHSFAOYNGVNGVNIOTNGPASIPIYDIDLGAFPSIDYYSADL 183  
 DB 175 VYRFRAGQYGTSMYSHSFAOYNGVNGVNIOTNGPASIPIYDIDLGAFPSIDYYSADL 234  
 QY 184 VELTKNSGAFSDNYLNFNGTAKHPETGESEYANVLTTPGRHRLRLINTSVENHFQVSLV 243  
 DB 235 VLLTGHAGSPNNVLFNFPAKHPTTGAGQYATVSLTKGKRRLRLINTSVENHFQVSLV 294  
 QY 244 NHTTCTIADMTVPVNMATVDSLFLVGORYDVYIEANRTPGYVWVNTFGSLCGGSRN 303  
 DB 295 NHTTCTIADMTVPVNMATVDSLFLVGORYDVYIEANRTPGYVWVNTFGGSKLGDSDN 354  
 QY 304 PYPALIFHAGAGPPTDEGKAPVDHNCGLDPLNKPVYARVPLSGFKAARDNLDTVL 363  
 DB 355 PYPALIFHAGAGPPTDEGKAPVDHNCGLDPLNKPVYARVPLSGFKAARDNLDTVL 414  
 QY 364 DTTGPTLFWYKNGSAININMGRAVVDYVLTQNTSPFPGYNIVEVNGADQMSWYLENDP 423  
 DB 415 DG-----FWYRVNGTAIINNMKPYLEYVLTGNTNVSQSDNIVQYEGVGMKYLENDP 469  
 QY 424 GAPFTLPHMHLGHDFYVLSRSPDESANRHYFDPARADGLSGANPVYRDVSMLEPA 483  
 DB 470 DGAFSLPHRHLGHDFYVLSRSPDESANRHYFDPARADGLSGANPVYRDVSMLEPA 529  
 QY 484 FGVVYLSFRADNPGANLFFCHITAMHVSGLGVYVLELRADLKGAVSDADADLRLCADM 543  
 DB 530 KMWLIAFTDNGSWLHCHITAMHVSGLGVYVLELRADLKGAVSDADADLRLCADM 589  
 QY 544 RRYWPTN-PPYKSDGLK 560  
 DB 590 RAYFPDNNAPFKDSDGLR 607  
 RESULT 3  
 LAC2\_NEUCR STANDARD; PRT; 619 AA.  
 AC P10574;

DT 01-JUL-1989 (Rel. 11, Created)  
 DT 01-FEB-1996 (Rel. 33, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Laccase precursor (BC 1.10.3.2) (Benzenediol:oxygen oxidoreductase)  
 DE (uricshiol oxidase) (laccase allele 75).  
 CN LACC.  
 OS Neurospora crassa.  
 OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;  
 OC Sordariales; Sordariaceae; Neurospora.  
 OX NCBI\_TaxID=5141;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=86087214; PubMed=2961749;  
 RA Germain U.A., Mueller G., Hunziker P.E., Larch K.;  
 RT Characterization of two allelic forms of Neurospora crassa laccase.  
 RL Amino- and carboxyl-terminal processing of a precursor.  
 J. Biol. Chem. 263:885-896(1988).  
 CC -1- FUNCTION: LIGNIN DEGRADATION AND DEOXYFICATION OF LIGNIN-DERIVED  
 PRODUCTS (PROBABLE).  
 CC -1- CATALYTIC ACTIVITY: 4 benzenediol + O(2) -> 4 benzenesemiquinone + 2  
 H(2)O.  
 CC -1- COFACTOR: BINDS 4 CU-IONS PER MOLECULE. THREE DISTINCT CU  
 CENTERS KNOWN AS TYPE 1 OR BLUE, TYPE 2 OR NORMAL, AND TYPE  
 3 OR COUPLED BINUCLEAR (BY SIMILARITY).  
 CC -1- SUBCELLULAR LOCATION: Secreted (Potential).  
 CC -1- SIMILARITY: BELONGS TO THE FAMILY OF MULTICOOPER OXIDASES.  
 CC -1- SIMILARITY: CONTAINS 3 PLASTOCYANIN-LIKE DOMAINS.  
 CC -----  
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 CC -----  
 DR EMBL: M18334; AAA33592.1; -.  
 DR PIR: B28523; KSNCLT.  
 DR InterPro: IPR001117; Cu-oxidase.  
 DR InterPro: IPR002355; Multicu\_oxidase2.  
 DR Pfam: PF00394; Cu-oxidase; 3.  
 DR PROSITE: PS00079; MULTICOOPER OXIDASE1; 1.  
 DR PROSITE: PS00080; MULTICOOPER OXIDASE2; 1.  
 KM Oxidoreductase; Signal; Copper; Metal-binding; Lignin degradation;  
 KM Glycoprotein; Repeat.  
 FT SIGNAL 1 21  
 FT PROPEP 22 49  
 FT CHAIN 50 606  
 FT PROPEP 607 619  
 FT DOMAIN 84 207  
 FT DOMAIN 216 373  
 FT DOMAIN 431 566  
 FT METAL 144 144  
 FT METAL 146 146  
 FT METAL 189 189  
 FT METAL 191 191  
 FT METAL 477 477  
 FT METAL 480 480  
 FT METAL 482 482  
 FT METAL 548 548  
 FT METAL 549 549  
 FT METAL 550 550  
 FT METAL 554 554  
 FT METAL 559 559  
 FT CARBOHYD 139 139  
 FT CARBOHYD 282 282  
 FT CARBOHYD 295 295  
 FT CARBOHYD 340 340  
 FT CARBOHYD 422 422  
 FT CARBOHYD 444 444  
 SQ SEQUENCE 619 AA; 68120 MW; 0BB6CDE18841145 CRC64;

Query Match

64.0%; Score 2021; DB 1; Length 619;

```

Db 333 GRSNNPFAAIIHYGASNSHPTNKGVAPADHECLDLNLVYVPRSLPTSGFVAASDNT 392
Qy 359 LDVLTDTGTPLFWKVGSAINIDGRAVDYVLTONTSPFPQYNIYEVNGADQMSYWL 418
Db 393 LDVQSTTRK---WTINGSTLDVDMGHPIYOYINKSTAMWSTDNVWLVEGANOMAYWL 449
Qy 419 IENDGAP-FITLPHPMHLGHDFYVLSGSPDESASNERHVDPAADGLSGANPVRD 477
Db 450 IENDPTAGNALPHPIHGHGDFVILGRSPNVSPTAQTPYTF-TSSDVSLSLGNPNIRRD 508
Qy 478 VSMLEPFGWVLSFRADNPGAWLFHCHIAHVSGLGVYTLERRADDLRAVSDADADD 537
Db 509 VMLPCKMLLAFTTPTGSAHMHCHIAHVSAGLSTFLEQPSAFVAGLNTDYNQNL 568
Qy 538 RLCAADRRYPTNP-YPKSDGL 559
Db 569 SQCKSMNAYTPSKDIFKDDSGV 591

RESULT 5
LACL BOTCI STANDARD; PRT: 486 AA.
ID LACL BOTCI
AC 012570:
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE Laccase (EC 1.10.3.2) (Benzenediol: oxygen oxidoreductase) (Urisiol
oxidase) (Diphenol oxidase) (Fragment).
GN LACL.
OS Botrytis cinerea (Botryotinia fuckeliana).
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Leotiomycetes;
OX Helotiales; Sclerotiales; Botryotinia.
RN NCBI_TaxID=40559;
RP [1]
RC SEQUENCE FROM N.A.
RA Cantone P.A.; Staples R.C.;
RT "A laccase cDNA from Botrytis cinerea.";
RL Phytopathology 83:1383-1385(1993).
CC -1- FUNCTION: LIGNIN DEGRADATION AND DETOXIFICATION OF LIGNIN-DERIVED
PRODUCTS (PROBABLE).
CC -1- CATALYTIC ACTIVITY: 4 benzenediol + O(2) -> 4 benzenesemiquinone + 2
H(2)O.
CC -1- COFACTOR: BINDS 4 CU-IONS PER MOLECULE. THREE DISTINCT CU
CENTERS KNOWN AS TYPE 1 OR BLUE, TYPE 2 OR NORMAL, AND TYPE
3 OR COUPLED BINUCLEAR (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: Secreted (Potential).
CC -1- SIMILARITY: BELONGS TO THE FAMILY OF MULTICOPPER OXIDASES.
CC -1- SIMILARITY: CONTAINS 3 PLASTOCYANIN-LIKE DOMAINS.
CC -1- CAUTION: THIS IS A CONCEPTUAL TRANSLATION; A STOP CODON HAD TO
BE SKIPPED IN POSITION 346 TO PRODUCE THIS ORF.
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CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@sib-sib.ch).
CC -----
DR EMBL: U20192; AAA41823.1; ALT_SEQ.
DR InterPro: IPR001117; Cu-oxidase.
DR InterPro: IPR002355; Multicopper oxidase.
DR Pfam: PF00394; Cu-oxidase; 3.
DR PROSITE: PS00079; MULTICOPPER OXIDASE2; 1.
DR PROSITE: PS00080; MULTICOPPER OXIDASE2; 1.
KM Oxidoreductase; Copper; Metal-binding; Lignin degradation;
FM Glycoprotein; Repeat.
FT NON_TER 1
FT DOMAIN <1 84 PLASTOCYANIN-LIKE 1.
FT DOMAIN 132 238 PLASTOCYANIN-LIKE 2.
FT DOMAIN 287 446 PLASTOCYANIN-LIKE 3.

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FT METAL 5 5 COPPER (TYPE 2) (BY SIMILARITY).
FT METAL 7 7 COPPER (TYPE 3) (BY SIMILARITY).
FT METAL 66 66 COPPER (TYPE 3) (BY SIMILARITY).
FT METAL 68 68 COPPER (TYPE 3) (BY SIMILARITY).
FT METAL 370 370 COPPER (TYPE 1) (BY SIMILARITY).
FT METAL 373 373 COPPER (TYPE 2) (BY SIMILARITY).
FT METAL 375 375 COPPER (TYPE 3) (BY SIMILARITY).
FT METAL 429 429 COPPER (TYPE 3) (BY SIMILARITY).
FT METAL 430 430 COPPER (TYPE 1) (BY SIMILARITY).
FT METAL 431 431 COPPER (TYPE 3) (BY SIMILARITY).
FT METAL 435 435 COPPER (TYPE 1) (BY SIMILARITY).
FT METAL 435 435 COPPER (TYPE 1) (BY SIMILARITY).
FT CARBOHYD 129 129 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 187 187 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 230 230 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 294 294 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 301 301 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 359 359 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 486 AA; 52567 MW; 19782C3E4108FE4D CRC64;

Query Match 26.1%; Score 824.5; DB 1; Length 486;
Best Local Similarity 34.4%; Pred. No. 2,1e-51;
Matches 176; Conservative 75; Mismatches 195; Indels 65; Gaps 12;

Qy 89 GTSIHWHGCHQKSTNLAHC-----ANCTECPIPPKGGKGVYRFRKAO 131
Db 1 GTTHMHGCHQKSTNLAHC-----ANCTECPIPPKGGKGVYRFRKAO 59
Qy 132 YGSMVHSHFSAOYGVGVGAIOINGPASPDTDGVPIPSYSSADELVELEKNSG 191
Db 60 YGSMVHSHFSAOYGVGVGAIOINGPASPDTDGVPIPSYSSADELVELEKNSG 119
Qy 192 APFSDVNLFGNGAKHPEDEGEYANTLTTPGRHRLRLINTSENFQVSLVNHWCITA 251
Db 120 PFTLLGLMNGTWTY--NGAGKKFQTFPGLKYRIRVNTAVDGHFQSIDGHSFOVIA 177
Qy 252 ADMVPPVNAATVDSLELGVQGRDVVEANRTGNTVFNTTFFGGGLCGSSRRPYP-AAIF 310
Db 178 MDEVPVPPVNAATVDSLELGVQGRDVVEANRTGNTVFNTTFFGGGLCGSSRRPYP-AAIF 235
Qy 311 HVAGARG-GPPDEKAPVDHNCIDLPNLKPVARVPVPSGFAKRDNTLDTLTGTGP 369
Db 236 RTYGSSSTADPTTTSVNTASTSLDEP-----LASLVPVPVPIPIASSIMKTTLTGGGQ 290
Qy 370 LEVWKGSAINIDGRAVDYVLTONTSPFPQYNIYEV-----NGAD 412
Db 291 ---WLENGSSILMTWDPDLTLVINGNIMPEYNYPIESTAKKGAVALAISGPNXA 347
Qy 413 QMSY---WLENDGAPFLTP-HPMHLGHDFYVLSGSPDESASNERHVPDPARAGLL 468
Db 348 FHYPPILLISNHTDMLFSSPNHPIHLGHGDFVTLISQGTGAATYAT-----AL 395
Qy 469 SGANPVRDVSMLEPFGWVLSFRADNPGAWLFHCHIAHVSGLGVYTLERRADDLRAV 528
Db 396 NLVNPFRDRLVLTSTGHLVIAFQIDNPGSWLMHCHIAHVSAGLSTFLEQPSAFVAGL 455
Qy 529 SDDADDDLRLCADRRYPTNPYPKSDGL 559
Db 456 GTADVSTFONTCAMKGMPTPEPFDSDGI 486

RESULT 6
LACL TRAVI STANDARD; PRT: 520 AA.
ID LACL TRAVI
AC 099044:
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE Laccase 1 precursor (EC 1.10.3.2) (Benzenediol: oxygen oxidoreductase)
(Diphenol oxidase).
GN LACL.
OS Trametes villosa (White-rot fungus).
OC Eukaryota; Fungi; Basidiomycota; Hymenomycetes; Homobasidiomycetes;

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CC -1- SIMILARITY: BELONGS TO THE FAMILY OF MULTICOPPER OXIDASES.
CC -1- SIMILARITY: CONTAINS 3 PLASTOCYANIN-LIKE DOMAINS.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; M60560; AAA33103.1; -.
DR EMBL; M60561; AAA33104.1; -.
DR PIR; A35883; A35883.
DR InterPro; IPR001117; Cu-oxidase.
DR InterPro; IPR002355; Multicopper oxidase2.
DR Pfam; PF00394; Cu-oxidase_3; Multicopper oxidase1.
DR PROSITE; PS00079; MULTICOPPER_OXIDASE2; FALSE_NEG.
DR PROSITE; PS00080; MULTICOPPER_OXIDASE2; FALSE_NEG.
KW Oxidoreductase; Signal; Copper; Metal-binding; Lignin degradation;
KW Glycoprotein; Repeat.
FT SIGNAL 1 21 POTENTIAL.
FT CHAIN 22 520 LACCASE.
FT DOMAIN 23 148 PLASTOCYANIN-LIKE 1.
FT DOMAIN 160 302 PLASTOCYANIN-LIKE 2.
FT DOMAIN 369 491 PLASTOCYANIN-LIKE 3.
FT METAL 85 85 COPPER (TYPE 2) (BY SIMILARITY).
FT METAL 87 87 COPPER (TYPE 3) (BY SIMILARITY).
FT METAL 130 130 COPPER (TYPE 3) (BY SIMILARITY).
FT METAL 132 132 COPPER (TYPE 3) (BY SIMILARITY).
FT METAL 416 416 COPPER (TYPE 1) (BY SIMILARITY).
FT METAL 419 419 COPPER (TYPE 2) (BY SIMILARITY).
FT METAL 421 421 COPPER (TYPE 3) (BY SIMILARITY).
FT METAL 473 473 COPPER (TYPE 1) (BY SIMILARITY).
FT METAL 474 474 COPPER (TYPE 3) (BY SIMILARITY).
FT METAL 475 475 COPPER (TYPE 3) (BY SIMILARITY).
FT METAL 479 479 COPPER (TYPE 1) (BY SIMILARITY).
FT METAL ? ? COPPER (TYPE 1) (BY SIMILARITY).
FT CARBOHYD 50 50 N-LINKED (GLCNAC . . . ) (POTENTIAL).
FT CARBOHYD 72 72 N-LINKED (GLCNAC . . . ) (POTENTIAL).
FT CARBOHYD 75 75 N-LINKED (GLCNAC . . . ) (POTENTIAL).
FT CARBOHYD 210 210 N-LINKED (GLCNAC . . . ) (POTENTIAL).
FT CARBOHYD 229 229 N-LINKED (GLCNAC . . . ) (POTENTIAL).
FT CARBOHYD 354 354 N-LINKED (GLCNAC . . . ) (POTENTIAL).
FT CARBOHYD 457 457 N-LINKED (GLCNAC . . . ) (POTENTIAL).
FT DISULFD 106 509 N-LINKED (GLCNAC . . . ) (POTENTIAL).
FT DISULFD 138 226 POTENTIAL.
FT VARIANT 411 411 POTENTIAL.
FT CONFLICT 378 379 SG -> R (IN REF. 1; AAA33104).
SQ SEQUENCE 520 AA; 55668 MW; 977DBDFA551F7929 CRC64;
Query Match 19.5%; Score 615; DB 1; Length 520;
Best Local Similarity 31.6%; Pred. No. 1.8e-36;
Matches 173; Conservative 73; Mismatches 212; Indels 90; Gaps 21.
Oy 37 TLTLEVNMTGPPDGVRKRYKLVNNSIIGPTIFDKMGTPIQVTVYNNEFN-----GSTI 92
| | | | | : | | : | | | | : | | : | | | | : | | | | |
Db 26 TADLTISNAEVSPPDFARQAV-VANNVTYGPFLVAGNKGRFDIYNIDNTIMLKSTSI 84
| | | | | | | | | | | : | | | | | : | | | | | : | | | | |
Oy 93 HWHGIHQKQTNIHDGANGITTECPTRPKGGKRYRKKA-QOQYSWYSHFSAOYGNGVYG 151
| | | | | | | | | | | : | | | | | : | | | | | : | | | | |
Db 85 HHWGFGOKTNNADPAFVNCPL-SGSISFLYDRQVPDQAGHFMYHSLSYQCGLRG 143
| | | | | | | | | | | : | | | | | : | | | | | : | | | | |
Oy 152 AIQI---NGPSALRPDTDLG--VFPISDYYSSADELYVELTKNSGARF---SDNYLFNGT 203
| | | | | | | | | | | : | | | | | : | | | | | : | | | | |
Db 144 PRVVVDPPNDPRASLDVDNDDTFITLADITRAA-----KLGAFFLAGDATATINEL 195
| | | | | | | | | | | : | | | | | : | | | | | : | | | | |
Oy 204 AKHPETGESEYNAVTLTPGRRHRLRLINTSVNHFEQVSLVNMTCMLTIADMPVNAATVD 263
| | | | | | | | | | | : | | | | | : | | | | | : | | | | |
Db 196 GSPSPSTAADIADVINTKKRFRRLVSLSCDPNRHFIISGDHLITIELVDSINSGLVAD 255
| | | | | | | | | | | : | | | | | : | | | | | : | | | | |
Oy 264 SLFLVGQRGVIVIANRTPGNTWF--NVTFGGGLCGSRNPDPRAITHYKAGAPGGPT 321
| | | | | | | | | | | : | | | | | : | | | | | : | | | | |
```

Db 256 SIQFEAQRYSFVLTNADQDVGNMYTRANPNNGNNGVFAGGIN-----SAILFYDGADPVEPT 311

QY 322 DEGAAPDHNCLDLPNPKPPVYARADYPLSGFAKKRADNLIDLTDTGTPLEFWKNGSAI- 380

Db 312 TTQTPPT--KELNVEVDLPLATMAVPPSPVAGVDLTALNMAFNNGTNFF--INGSEV 366

QY 381 --NIDMGAVVDYVLTQNTSEPPG--NVIYEVNCAADQSYMLIENDPCAPETLPHPMILH 436

Db 367 PPVYPLVLLQITISAGNMADLLPSGSVYSLPS-NMDIELSPFATAARCA-----PHPEFLH 421

QY 437 GHDFVYLGSRPDESPASNERHVEPDARDAG--LLSGANPERDY--SKLPAPG-WVYLSE 491

Db 422 GHAFVY-----RSAGSTVYNITNDFPRDVSSTGTGPAAGNVITRF 462

QY 492 RADNPAGWLFFCHIAMHYSGLGVYVYLERADLDGAVSDADADLDRLCADWRRYPTNP 551

Db 463 RTDNPGRFFLCHIDHLEAGFAVFAEDIDVASA-----NP 500

QY 552 YPKSDSGL 559

Db 501 VPQAWSDL 508

RESULT 8

LAC4\_TRAVI STANDARD: PRT; 520 AA.

ID LAC4\_TRAVI

AC Q09055;

DT 01-NOV-1997 (Rel. 35, Created)

DT 01-NOV-1997 (Rel. 35, Last sequence update)

DT 01-NOV-1997 (Rel. 35, Last annotation update)

DE Laccase 4 precursor (EC 1.10.3.2) (benzenediol: oxygen oxidoreductase)

DE (Urishiol oxidase) (Diphenol oxidase).

GN LCC4.

OS Trametes villosa (White-rot fungus).

OC Eukaryota; Fungi; Basidiomycota; Hymenomycetes; Homobasidiomycetes;

OC Asphyliophorales; Trametes.

OX NCBI\_TaxID=47662;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=97128774; PubMed=8973314;

RA Yaver D.S., Gollightly E.J.;

RT "Cloning and characterization of three laccase genes from the

RT white-rot basidiomycete Trametes villosa: genomic organization of the

RT laccase gene family";

RL Gene 181;95-102(1996).

CC -1- FUNCTION: LIGNIN DEGRADATION AND DETOXIFICATION OF LIGNIN-DERIVED

CC PRODUCTS (PROBABLE).

CC -1- CATALYTIC ACTIVITY: 4 benzenediol + O(2) = 4 benzosemiquinone + 2

CC H(2)O.

CC -1- COFACTOR: BINDS 4 CU-IONS PER MOLECULE, THREE DISTINCT CU

CC CENTERS KNOWN AS TYPE 1 OR BLUE, TYPE 2 OR NORMAL, AND TYPE

CC 3 OR COUPLED BINUCLEAR (BY SIMILARITY).

CC -1- SUBUNIT: HOMODIMER (BY SIMILARITY).

CC -1- SUBCELLULAR LOCATION: Secreted.

CC -1- SIMILARITY: BELONGS TO THE FAMILY OF MULTICOPPER OXIDASES.

CC -1- SIMILARITY: CONTAINS 3 PLASTOCYANIN-LIKE DOMAINS.

CC -----

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CC -----

CC EMBL; L78077; AAB47734.1; -.

DR HSSP; P37064; IASO.

DR InterPro; IPR001117; Cu-oxidase.

DR InterPro; IPR002355; Multicu\_oxidase2.

DR Pfam; PF00394; Cu-oxidase; 3.

DR PROSITE; PS00079; MULTICOPPER\_OXIDASE1; 1.

DR PROSITE; PS00080; MULTICOPPER\_OXIDASE2; FALSE\_NEG.

DR Oxidoreductase; Signal; Copper; Metal-binding; Glycoprotein; Repeat;

FW

FT	CABOND	497	497	N-LINKED (G/C/NAC. . .) (POTENTIAL).
SQ	SEQUENCE	520 AA;	55643 MW;	EC1032400E9DDFAA CXC64;
	Query Match		19.1%;	Score 602; DB 1; Length 520;
	Best Local Similarity		32.0%;	Pred. No. 1.5e-35;
	Matches 179;	Conservative	77;	Mismatches 211; Indels 92; Gaps 24;
QY	30	TCGVNPPY-LTLEEDNMTGPGGVYKEKYMVNNSIIGPTIADMGDITQVTVINNL--E	86	
DB	21	SAAGPVTDLTISNAD--VSPDGFTRAVY-LANGVFPGGLITGNKGDNFQIVIDLNSNE	77	
QY	87	T--NCTSIHHMGLHCKGTNLNHDGANGITECPIPPKGRKVVYEFKA-QOYGISWYHSFSA	143	
DB	78	TMLKSTSIHHMGHFPQGTNNMADGAFAVNOCPY-ATGNSFLYDFATADAGTFWYHSHST	136	
QY	144	OYGNGVYCAIQINGNASLPY-----DDLDGFFPISDYVYSSADELVETKNSGAP---	194	
DB	137	QYCDLRKRPVYVYDPSD--PHADLYVDDETITLTSLDMYHFA-----SLGAAPIG	187	
QY	195	SDNVLENGTAKHPTEGESEYANVTLTGPRNRLRLINTSVENHFOVSLVHFMCIITADN	254	
DB	188	SDSTLNLGRRAGGDSYDLAVITVEQGRKRYMRMLSLSCDPNYVFSIDGHMNTIIEADA	247	
QY	255	VPVNAMYVDSLFLVGQGRDYVTEANKTPGNTWF-----NVTFGGGLCGGSRNPYPA	307	
DB	248	VNHEPLTADYSIQIYVGQYSEFLTGADODIDNFIYALPSAGTTSFGGI-----NS	298	
QY	308	ALFHHAGAGGPPDEGRAPVDHNCGLDIPNKKPVAROVPLSGFPAKRAADNTLDVLTDTG	367	
DB	299	ALIKRSGASEVDPTTETTSV--LPIDENALVPLDSPAPAGDPNIGGVADYALNIDPNFDG	356	
QY	368	TPLEPVKNGSAINIDWGRAVVDYVLTGNTS---FPPG-YNIVEVNGADQMSYML-IEB	421	
DB	357	TNFFINDVSFVSPVY----PVLLQISGTSADLLPSSGLPALPSNSTIEISFPITATN	412	
QY	422	DGAGFTLPHPMHILGHDFYVIGRSPDSESPASNEHNVDPDANDAGL--LSGANPVRDYS	479	
DB	413	APGA---PHPHLLGHFSTV-----RTASGTDTPNFNPPVRDYY	449	
QY	480	MLPAFG-WVYLSFRADNGAMFLFCHIAMHVSGLGVYLERADDLRGAVSDADDDDLR	538	
DB	450	NTGFGADVNTIRFTDNDQPMFLHCHIDPHELAGPAIVSEEDTADVSNTTPTSTA-----	504	
QY	539	LCADMRRKRYWPT-NRYPKSD	556	
DB	505	---MEDLCPTYNALDSSD	519	
RESULT 10				
LACS_TRAVI				
ID	LACS_TRAVI	STANDARD:	PRT:	527 AA.
AC	Q09056;			
DT	01-NOV-1997 (Rel. 35, Created)			
DT	16-OCT-2001 (Rel. 40, Last sequence update)			
DT	16-OCT-2001 (Rel. 40, Last annotation update)			
DE	Laccase 5 precursor (EC 1.10.3.2) (Benzenediol: oxygen oxidoreductase)			
DE	(Urishiol oxidase).			
GN	LCC5.			
OS	Trametes villosa (White-rot fungus).			
OC	Eukaryota; Fungi; Basidiomycota; Hymenomycetes; Homobasidiomycetes;			
OC	Agaricomycetes; Basidiomycetes; Basidiomycota; Hymenomycetes; Homobasidiomycetes;			
OC	Agaricomycetes; Basidiomycetes; Basidiomycota; Hymenomycetes; Homobasidiomycetes;			
OX	NCBI_TaxID=47662;			
RP	SEQUENCE FROM N.A.			
RP	MEDLINE=97128774; PubMed=8973314;			
RA	Yaver D.S., Gollightly E.J.;			
RT	"Cloning and characterization of three laccase genes from the			
RT	white-rot basidiomycete Trametes villosa: genomic organization of the			
RT	laccase gene family."			
RL	Gene 181:95-102(1996).			
RP	REVISIONS.			
RA	Yaver D.S., Gollightly E.J.;			

BL Submission (JAN-2001) to the EMBL/GenBank/DDBJ databases.

CC -1- FUNCTION: LIGNIN DEGRADATION AND DETOXIFICATION OF LIGNIN-DERIVED PRODUCTS (PROBABLE).

CC -1- CATALYTIC ACTIVITY: 4 benzenediol + O(2) = 4 benzosemiquinone + 2 H(2)O.

CC -1- COFACTOR: BINDS 4 CU-IONS PER MOLECULE. THREE DISTINCT CU CENTRES KNOWN AS TYPE 1 OR BLUE, TYPE 2 OR NORMAL, AND TYPE 3 OR COUPLED BINUCLEAR (BY SIMILARITY).

CC -1- SUBUNIT: HOMODIMER (BY SIMILARITY).

CC -1- SUBCELLULAR LOCATION: Secreted.

CC -1- SIMILARITY: BELONGS TO THE FAMILY OF MULTICOOPER OXIDASES.

CC -1- SIMILARITY: CONTAINS 3 PLASTOCYANIN-LIKE DOMAINS.

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```
DR EMBL: L78078; ABAB7735.2; -.
DR HSSP; P37064; IAOZ.
DR InterPro; IPRO01117; Cu-oxidase.
DR InterPro; IPRO02355; Multicu_oxidse2.
DR Pfam; PF00394; Cu-oxidase; 3.
DR PROSITE; PS00079; MULTICOOPER_OXIDASE1; 1.
DR PROSITE; PS00080; MULTICOOPER_OXIDASE2; FALSE_NEG.
KW Oxidoreductase; Signal; Copper; Metal-binding; Glycoprotein; Repeat;
FT Lignin degradation; Multigene family.
FT SIGNAL 1 23
FT CHAIN 24 527
FT FTT 25 150
FT FTF DOMAIN 162 306
FT FTH DOMAIN 373 498
FT FTL METAL 87 87
FT FTM METAL 89 89
FT FTN METAL 132 132
FT FTO METAL 134 134
FT FTV METAL 425 425
FT FTT METAL 428 428
FT FTS METAL 430 430
FT FTR METAL 480 480
FT FTD METAL 481 481
FT FTE METAL 482 482
FT FTF METAL 486 486
FT FTH METAL ? ?
FT FTI METAL ? ?
FT FTK CARBOHYD 74 74
FT FTL CARBOHYD 77 77
FT FTM CARBOHYD 156 156
FT FTN CARBOHYD 209 209
FT FTO CARBOHYD 233 233
FT FTV CARBOHYD 242 242
FT FTT CARBOHYD 276 276
FT FTS CARBOHYD 317 317
FT FTR CARBOHYD 358 358
FT FTD CARBOHYD 366 366
FT FTE CARBOHYD 393 393
FT FTF CARBOHYD 402 402
FT FTH CARBOHYD 464 464
FT FTI CARBOHYD 527 AA; 56247 MW; FLBB638D65FFA478 CRC64;
SQ SEQUENCE
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Query Match 18.5%; Score 563.5; DB 1; Length 537;  
Best Local Similarity 30.5%; Pred. No. 3,2e-34;  
Matches 178; Conservative 66; Mismatches 202; Indels 137; Gaps 26;

Oy	31	GVAEYRT--LTLEEVNMWGPDGVEAEKVALVNNSITGIPTFADMCDTQIVINN--ET	87
	:: :	:	:
Dd	23	GALGVDTDLTISNAD--VTPDSITRAAV--LAGGVPPGLPIGTGNKKDEQINVINDM/TNET	79
	:	:	:
Oy	88	--NGTSHHMGILHGKGTNLHDGANGITCEPLDPKGGKGRKYRKA-QQGTSTYSHFSQA	144
	:::::: :	:	: :
Dd	80	MUKSTTHHHGFLFGAGTWNADGAAPVNCPI-ATGNSFLYDTVPDQAGTFTYHSHLSTQ	138
	:: :	:	: :



Db 355 SFSNGSNFNNETFPVTVLQILSGADASLNGSV-----YTLPSNS 403

Qy 398 SFPQGVNIVEVNGADQMSWYLNDPGAPFTLPHPMHLGHDFVLGRSPDESPASNERH 457

Db 404 TIEISFTITTDGA-----LNAPGA-----PHEFLHGHTEFSV----- 437

Qy 458 VFEDARQAG--LLSGANPVARD--VSMLEPFGWYLSFADNPGAMFLFCHTAMHVSGLG 514

Db 438 -----RSAGSSTFVNANVRDVTGNSGDNVTLRFTTDPNGPWFELHCHIDFILDAGFA 492

Qy 515 VVLERADDLRGAVSDADADLRLCADRRKRYPTNPYKSDS 557

Db 493 IVFAE-----DTADTASANPPTPAMSOLCPT--YDALDS 524

RESULT 12

LAC2\_TRAVE STANDARD; PRT; 519 AA.

ID LAC2\_TRAVE

AC 099046;

DT 01-NOV-1997 (Rel. 35, Created)

DT 01-NOV-1997 (Rel. 35, Last sequence update)

DT 15-JUL-1998 (Rel. 36, Last annotation update)

DE Laccase 2 precursor (EC 1.10.3.2) (Benzenediol: oxygen oxidoreductase)

GN (Uristiol oxidase) (Diphenol oxidase).

OS LCC2.

OC Trametes villosa (white-rot fungus).

OC Eukaryote; Fungi; Basidiomycota; Hymenomycetes; Homobasidiomycetes;

OC Aphyllophorales; Trametes.

OX NCBI\_TaxId=47662;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE=Mycelium.

RX MEDLINE=97076915; PubMed=8975613;

RA Yaver D.S., Xu F., Gollighly E.J., Brown K.M., Brown S.H.,

RA Ray M.W., Schneider P., Halkier T., Mondorf K., Dalboge H.;

RT "Purification, characterization, molecular cloning, and expression of

RT two laccase genes from the white rot basidiomycete Trametes

RT villosa.";

RL Appl. Environ. Microbiol. 62:834-841(1996).

CC -1- FUNCTION: LIGNIN DEGRADATION AND DETOXIFICATION OF LIGNIN-DERIVED

CC PRODUCTS (PROBABLE).

CC -1- CATALYTIC ACTIVITY: 4 benzenediol + O(2) -> 4 benzoquinone + 2

CC H(2)O.

CC -1- COFACTOR: BINDS 4 CU-IONS PER MOLECULE. THREE DISTINCT CU

CC CENTERS KNOWN AS TYPE 1 OR BLUE, TYPE 2 OR NORMAL, AND TYPE

CC 3 OR COUPLED BINOCLEAR (BY SIMILARITY).

CC -1- SUBUNIT: HOMODIMER.

CC -1- SUBCELLULAR LOCATION: Secreted.

CC -1- SIMILARITY: BELONGS TO THE FAMILY OF MULTICOPPER OXIDASES.

CC -1- SIMILARITY: CONTAINS 3 PLASTOCYANIN-LIKE DOMAINS.

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CC -----

CC EMBL: LA9377; AAC41687.1; .

CC HSSP: P37064; LAOZ.

DR InterPro: IPR001117; Cu-oxidase.

DR InterPro: IPR002355; MulticCu\_oxidase2.

DR Pfam: PF00394; Cu-oxidase; 3.

DR PROSITE: PS00079; MULTICOPPER\_OXIDASE1; 1.

DR PROSITE: PS00080; MULTICOPPER\_OXIDASE2; FALSE\_NEG.

KM Oxidoreductase; Signal; Copper; Metal-binding; Glycoprotein; Repeat;

KM Lignin degradation; Multigene family.

FT SIGNAL 1 20 POTENTIAL.

FT CHAIN 21 519 LACCASE 2.

FT DOMAIN 22 147 PLASTOCYANIN-LIKE 1.

FT DOMAIN 159 301 PLASTOCYANIN-LIKE 2.

FT DOMAIN 368 490 PLASTOCYANIN-LIKE 3.

FT METAL 84 84 COPPER (TYPE 2) (BY SIMILARITY).

FT METAL 86 86 COPPER (TYPE 3) (BY SIMILARITY).

FT METAL 129 129 COPPER (TYPE 3) (BY SIMILARITY).

FT METAL 131 131 COPPER (TYPE 3) (BY SIMILARITY).

FT METAL 415 415 COPPER (TYPE 1) (BY SIMILARITY).

FT METAL 418 418 COPPER (TYPE 2) (BY SIMILARITY).

FT METAL 420 420 COPPER (TYPE 3) (BY SIMILARITY).

FT METAL 472 472 COPPER (TYPE 3) (BY SIMILARITY).

FT METAL 473 473 COPPER (TYPE 1) (BY SIMILARITY).

FT METAL 474 474 COPPER (TYPE 3) (BY SIMILARITY).

FT METAL 478 478 COPPER (TYPE 1) (BY SIMILARITY).

FT METAL 7 7 COPPER (TYPE 1) (BY SIMILARITY).

FT CARBOHYD 74 74 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 161 161 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 228 228 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 237 237 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 271 271 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 353 353 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 361 361 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 456 456 N-LINKED (GLCNAC. . .) (POTENTIAL).

SQ SEQUENCE 519 AA; 55777 MM; DB4EA526F684740 CRC64;

Query Match 18.1%; Score 571; DB 1; Length 519;

Best Local Similarity 29.7%; Pred. No. 2,5e-33;

Matches 162; Conservative 75; Mismatches 200; Indels 108; Gaps 22;

Qy 49 PDGVKREKVMVNNSSIPTIFADWDGTIQYVINNLFTN-----CTSIHMHGLHOKGTNL 104

Db 37 PDGFLRDAL-VVNGVVPRLITGKKGRFQLNVYDTLNNHSMKSTSIHMGFRAGTNW 95

Qy 105 HDGANGITECPPIPKGGRKRYRFXA-QOYGTWSHSPSAOYGNCGVAIOI---NGPAS 160

Db 96 AEGPAFVNCPI-ASGHSELYDFHVPDQAGTFYHSHSLSTGYCQDLRSPFYVYPRKDHA 154

Qy 161 LPTPTD--LGFPISDYYSADDELVELTKNSGAF---SDNVLENGAKHPGESEYTA 215

Db 155 SRIDVNESTVITLIDWHTIA-----RLGKPEPLGADVTLLNGSRASSTYALA 206

Qy 216 NVTLTPGRHRLRLINTSVENHFOVSLVNHHTCITADNVVNATVSLFVGQORYDV 275

Db 207 VINQHGKRYRFLVLSICDNYTFSDIGNHLVIEVDGINSQPLVDISQIFAAQRSSF 266

Qy 276 VIEAKRTGTNWF--NTFPGGLCGSRNPPAIFRYAGAPGPPDEGKAPVDNCL 333

Db 267 VLNMQTGNWVRANPFGVGFAGIN---SAILTYOGAPVAEPPTTQTPSV----- 317

Qy 334 DLP-----NLKPVVADVPLSGFAKRAADNTLDYDTTGTPLPFVKNVNGSA-----I 380

Db 318 -IPLETLHLHLPVPGSTPPGCVDAKALNAFENGTNF---INNAITPTPTVPVL 373

Qy 381 NIDGRAVVDVLTQNTSP-PGYNIVEVNGADQMSWYLNDPGAPFTLPHPMHLGHGD 439

Db 374 QILSGAQAOQLDLAGSVYPLPAHSTIEI-----TLPATLAPGA-----PHEFLHGH 423

Qy 440 FVYGRSDESPASERKRVFDPARAG--LLSGANPVARDV--SMLEPFG--WVLSFAD 494

Db 424 FAVV-----RSAGSTYNYNDPIRDVASTPAPAGDNVTLRFQTD 464

Qy 495 NPGAMLFCHTAMHVSGLIGVYLERADDLRGAVSDADADLRLCADRRKRYPTNPYK 554

Db 465 NPGWFLHCHIDFILDAGFAIVFAEDADVAKA-----NPPPK 502

Qy 555 SDSGL 559

Db 503 AMSDL 507

RESULT 13

LAC2\_TRAVE STANDARD; PRT; 519 AA.

ID LAC2\_TRAVE

AC 012718; 012716;

DT 01-NOV-1997 (Rel. 35, Created)

DT 01-NOV-1997 (Rel. 35, Last sequence update)



CC -1- COFACTOR: BINDS 4 CU-IONS PER MOLECULE. THREE DISTINCT CU  
CC CENTERS KNOWN AS TYPE 1 OR BLUE, TYPE 2 OR NORMAL, AND TYPE  
CC 3 OR COUPLED BINUCLEAR (BY SIMILARITY).  
CC -1- SUBUNIT: HOMODIMER (BY SIMILARITY).  
CC -1- SUBCELLULAR LOCATION: Secreted.  
CC -1- TISSUE SPECIFICITY: IN MYCELSIA, AT A LOWER LEVEL THAN LCC4.  
CC -1- SIMILARITY: BELONGS TO THE FAMILY OF MULTICOPPER OXIDASES.  
CC -1- SIMILARITY: CONTAINS 3 PLASTOCYANIN-LIKE DOMAINS.  
CC  
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CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
CC  
CC EMBL: Z54215; CAA9042.1. -  
CC InterPro: IPR001117; Cu-oxidase.  
CC InterPro: IPR003355; Multicu\_oxidase2.  
CC DR Pfam: PF00394; Cu-oxidase.3.  
CC DR PROSITE: PS00079; MULTICOPPER OXIDASE1. 1.  
CC DR PROSITE: PS00080; MULTICOPPER OXIDASE2. FALSE NEG.  
CC Oxidoreductase; signal; copper; Metal-binding; Glycoprotein; Repeat;  
CC Lignin degradation; Multigene family; Polymorphism.  
CC  
CC SIGNAL 1  
CC CHAIN 18  
CC FT 19 572  
CC FT DOMAIN 21 145 PLASTOCYANIN-LIKE 1.  
CC FT DOMAIN 157 304 PLASTOCYANIN-LIKE 2.  
CC FT DOMAIN 422 540 PLASTOCYANIN-LIKE 3.  
CC FT METAL 82 84 COPPER (TYPE 2) (BY SIMILARITY).  
CC FT METAL 84 84 COPPER (TYPE 3) (BY SIMILARITY).  
CC FT METAL 127 127 COPPER (TYPE 3) (BY SIMILARITY).  
CC FT METAL 129 129 COPPER (TYPE 3) (BY SIMILARITY).  
CC FT METAL 470 470 COPPER (TYPE 1) (BY SIMILARITY).  
CC FT METAL 473 473 COPPER (TYPE 2) (BY SIMILARITY).  
CC FT METAL 475 475 COPPER (TYPE 3) (BY SIMILARITY).  
CC FT METAL 522 522 COPPER (TYPE 3) (BY SIMILARITY).  
CC FT METAL 523 523 COPPER (TYPE 1) (BY SIMILARITY).  
CC FT METAL 524 524 COPPER (TYPE 1) (BY SIMILARITY).  
CC FT METAL 528 528 COPPER (TYPE 1) (BY SIMILARITY).  
CC FT METAL ? ? COPPER (TYPE 1) (BY SIMILARITY).  
CC FT CARBOHYD 182 182 N-LINKED (GLCNAC. . .) (POTENTIAL).  
CC FT CARBOHYD 228 228 N-LINKED (GLCNAC. . .) (POTENTIAL).  
CC FT CARBOHYD 294 294 N-LINKED (GLCNAC. . .) (POTENTIAL).  
CC FT CARBOHYD 367 367 N-LINKED (GLCNAC. . .) (POTENTIAL).  
CC FT CARBOHYD 405 405 N-LINKED (GLCNAC. . .) (POTENTIAL).  
CC FT VARIANT 159 159 D -> N.  
CC FT VARIANT 359 359 R -> H.  
CC FT VARIANT 418 418 H -> Y.  
CC FT VARIANT 448 448 I -> V.  
CC FT VARIANT 572 572 I -> V.  
CC SQ SEQUENCE 572 AA; 63747 MW; DFLZAPF9F108CE4 CRC64;

Query Match 17.9%; Score 565; DB 1; Length 572;  
Best Local Similarity 31.2%; Pred. No. 7.4e-33;  
Matches 116; Conservative 60; Mismatches 206; Indels 122; Gaps 22;

QY 49 PDGVKKEKMLVNNISLPTFADMDGLTYVTVNNLETN-----GTSIHMGHLQKGTN 103  
DB 35 PDGVERD-ATLVNGYGPGLFANKGDTLKYVONKL-TNPDMDRTTISIHMGHLQHNNA 92  
QY 104 LHQGANITCEPRPKGGRKYRKAAQOYGTSMYSHPSAQYGVGAIDINGPASLPY 163  
DB 93 DDDGPAVTCOPPIVPOASVYTYMPLGSDTGYWYHSHSSQYVGLRGRLVYDPKD-PH 151  
QY 164 -----DTDGVFPIISYYYSAADELVELTKNSGAPSDNVLENG-----TAKHPET 209  
DB 152 RLALYDIDKVTLLITGMYHRSKAIL-ATGNITLLQOPDSATTKGGRPDNDTPANNNT 210  
QY 210 GEGEVANTLTGRRHRLRLINTSVENHFQVSLVNHHTCCILADMDVPVNAVTVSLFLGV 269  
DB 211 -----LYTLKVRKGRKRYRLRVAINSSAISFRMSIGGKMTVIAADGVSTKRPQVDSFDLA 266

QY 270 GORDVIVIANRTPGNWYFNV-----TEGGILCGGSRNPY-----PAAI 309  
DB 267 GORDAIVAEVNEDEPTVWYNAPLVNANKTAQALLIEDDRPYPHPRGPKRMSVSEAI 326  
QY 310 FHYACAPGCPPTDEG-----KAPVDHNCIDLPLKRVVARD-----VLS-G 350  
DB 327 IKYWKHKRGRLSLGSHGGLKARMEGSLHLGRDRIVKRONETTVVMDKTVLEHFG 386  
QY 351 FA-----KRADNTLDVTLD-----TTCGFLFYKVNKG-----SAINIDGRAVVDY 392  
DB 387 AACGSRPDLVIDLTFYGNFTTG-----WMINGIRHKSPDMFTLKLITDTSVTSDFY 442  
QY 393 LVQNTSPFGYNYEVNGADOMSYWLINDPAPPLPMPHLHGHDFYVL--GRSPDES 450  
DB 443 QPETHILPKKNCVFEFN-----IKNGSG--LGIVHPHILHGHTEFDVVGFGNNP-- 489  
QY 451 PASNRHVPDARADAGLSGANPVRDVSMLPFGVYLSFPADNPGMALFCHIAHVS 510  
DB 490 -----NYNPPRRDVGATDEG-VRFQFTDNDPFWFLCHIDWHILE 530  
QY 511 GLGVYLERADDLRGAVSDADAD 534  
DB 531 EGFANVFANAEPAIKGPKSVYVD 554

RESULT 15  
LAC4\_THACU  
ID LAC4\_THACU STANDARD; PRT; 531 AA.  
AC 002081;  
DT 01-NOV-1997 (Rel. 35, Created)  
DT 01-NOV-1997 (Rel. 35, Last sequence update)  
DT 15-JUL-1999 (Rel. 38, Last annotation update)  
DE Laccase 4 precursor (EC 1.10.3.2) (benzenediol:oxygen oxidoreductase)  
GN (Trishiol oxidase) (Diphenol oxidase).  
OS Thanatephorus cucumeris (Black scurf of potato) (Rhizoctonia solani).  
OC Eukaryota; Fungi; Basidiomycota; Hymenomycetes; Heterobasidiomycetes;  
OC Heterobasidiomycetidae; Ceratobasidiales; Ceratobasidiaceae;  
OC Mitosporic Ceratobasidiaceae; Rhizoctonia.  
OX NCBI\_Taxid=107832;  
RN [1]  
RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.  
RC STRAIN-RS22;  
RX MEDLINE=96171523; PubMed=8598061;  
RA Halkier T., Kauppinen S., Pederson A., Schneider P.;  
RA Halkier T., Kauppinen S., Pederson A., Schneider P.;  
RT "The identification and characterization of four laccases from the  
RT plant pathogenic fungus Rhizoctonia solani.";  
RL Curr. Genet. 29:395-403(1996).  
CC -1- FUNCTION: LIGNIN DEGRADATION AND DETOXIFICATION OF LIGNIN-DERIVED  
CC PRODUCTS (PROBABLE). THIS ISOZYME SHOWS OPTIMAL ACTIVITY AT PH 7.  
CC -1- CATALYTIC ACTIVITY: 4 benzenediol + O(2) -> 4 benzenesulfinone + 2  
CC H(2)O.  
CC -1- COFACTOR: BINDS 4 CU-IONS PER MOLECULE. THREE DISTINCT CU  
CC CENTERS KNOWN AS TYPE 1 OR BLUE, TYPE 2 OR NORMAL, AND TYPE  
CC 3 OR COUPLED BINUCLEAR (BY SIMILARITY).  
CC -1- SUBUNIT: HOMODIMER.  
CC -1- SUBCELLULAR LOCATION: Secreted.  
CC -1- TISSUE SPECIFICITY: IN MYCELSIA, AT A HIGHER LEVEL THAN LCC1, LCC2  
CC AND LCC3.  
CC -1- SIMILARITY: BELONGS TO THE FAMILY OF MULTICOPPER OXIDASES.  
CC -1- SIMILARITY: CONTAINS 3 PLASTOCYANIN-LIKE DOMAINS.  
CC  
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CC  
CC EMBL: Z54277; CAA91042.1. -  
CC InterPro: IPR001117; Cu-oxidase.

GenCore version 5.1.3  
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OM protein - protein search, using sw model

Run on: December 4, 2002, 10:45:46 ; Search time 39 Seconds  
(without alignments)  
3027.308 Million cell updates/sec

Title: US-09-869-877-10

Perfect score: 3158  
Sequence: 1 QQSCNTPNSNRACWTDGXDIN.....KSDSGIKHRVGEGLVYKA 573

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

SPTREMBL\_21:\*  
1: sp.\_archaea:\*  
2: sp.\_bacteria:\*  
3: sp.\_fungi:\*  
4: sp.\_human:\*  
5: sp.\_invertebrate:\*  
6: sp.\_mammal:\*  
7: sp.\_mnc:\*  
8: sp.\_organelle:\*  
9: sp.\_phage:\*  
10: sp.\_plant:\*  
11: sp.\_rodent:\*  
12: sp.\_virus:\*  
13: sp.\_vertebrate:\*  
14: sp.\_unclassified:\*  
15: sp.\_virus:\*  
16: sp.\_bacteriophage:\*  
17: sp.\_archaeal:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1523	48.2	581	3	08TFE2
2	1461.5	46.3	589	3	09C497
3	1113.5	35.3	454	3	096UM2
4	1071.5	33.9	581	3	096UM9
5	974.5	30.2	561	3	096UM0
6	954	30.9	608	3	08TFE4
7	953.5	30.8	607	3	08TFE1
8	940.5	29.8	578	3	08TFD9
9	929.5	29.4	578	3	08TFE3
10	856.5	27.1	605	3	000292
11	662	21.0	436	3	096UQ0
12	661.5	20.9	437	3	096UP8
13	645	20.4	520	3	013448
14	640	20.3	520	3	096UT7
15	636	20.1	520	3	08TFM1
16	634	20.1	520	3	094222

17	628	19.9	520	3	08TG94	08tg94	trametes pu
18	620.5	19.6	518	3	074171	074171	schizophyll
19	619	19.6	520	3	013421	013421	basidiomyc
20	614	19.4	539	3	099780	099780	coprinus cl
21	611	19.3	520	3	059944	059944	ceriporiops
22	609	19.3	518	3	096TR6	096tr6	psycnoporus
23	607	19.2	538	3	096VAV5	096vav5	psycnoporus
24	606	19.2	533	3	060199	060199	pleurotus o
25	604.5	19.2	524	3	013422	013422	basidiomyc
26	599.5	19.0	526	3	08TF93	08tf93	trametes pu
27	593	18.8	423	3	096UQ1	096uq1	fusarium pr
28	593	18.8	518	3	059896	059896	psycnoporus
29	590.5	18.7	477	3	09HDS7	09hds7	polyporus c
30	590.5	18.7	524	3	09HDS8	09hds8	polyporus c
31	590	18.7	517	3	09Y781	09y781	coprinus cl
32	588	18.6	518	3	09UVO2	09uvo2	psycnoporus
33	587.5	18.6	424	3	096UP9	096up9	fusarium pr
34	587	18.6	519	3	013420	013420	basidiomyc
35	584.5	18.5	411	3	096V70	096v70	fusarium pr
36	584	18.5	526	3	013456	013456	coriolus ve
37	581.5	18.4	517	3	09HDS0	09hds0	trametes tr
38	580	18.4	517	3	09P8G4	09p8g4	coriolopsis
39	578	18.3	516	3	09Y782	09y782	coprinus cl
40	575.5	18.2	518	3	09HDS9	09hds9	polyporus c
41	573.5	18.2	518	3	08WZG3	08wzg3	lentiniula e
42	567.5	18.0	517	3	012571	012571	basidiomyc
43	567.5	18.0	517	3	09UVO5	09uvo5	marasmius q
44	562	17.8	518	3	08TFE8	08tf8	coriolus hl
45	561	17.8	519	3	096UK8	096uk8	trametes ve

## ALIGNMENTS

### RESULT 1

08TFE2 ID 08TFE2 PRELIMINARY: PRT: 581 AA.

AC 08TFE2; DT 01-JUN-2002 (TREMBLrel. 21, Created)

DT 01-JUN-2002 (TREMBLrel. 21, Last sequence update)

DE 01-JUN-2002 (TREMBLrel. 21, Last annotation update)

GN Lacase precursor (EC 1.10.3.2).

OS Gaeananomyces graminis var. tritici.

OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;

OC Sordariomycetes; Incertae sedis; Magnaporthaceae; Gaeananomyces.

OX NCBI\_TaxID=36779;

RN [1] SEQUENCE FROM N.A.

RX MEDLINE-21861250; PubMed-11872481;

RA Litvinseva A.P.; Henson J.M.;

RT Cloning, characterization, and transcription of three lacase genes from Gaeananomyces graminis var. tritici, the take-all fungus.;

RL Appl. Environ. Microbiol. 68:1305-1311(2002).

RN [2] SEQUENCE FROM N.A.

RA Litvinseva A.P.;

RT Genetics of lacase in Gaeananomyces graminis, the Take-All

RL Thesis (2002), Department of Microbiology,

RL Montana State University-Bozeman, Bozeman, USA.

DR EMBL; AJ417687; CAD10749.1; -

KW Signal; Oxidoreductase.

FT SIGNAL 1 14 POTENTIAL.

SQ SEQUENCE 581 AA; 64255 MW; ABF21F551BC039A1 CRC64;

Query Match 48.2%; Score 1523; DB 3; Length 581;

Best Local Similarity 53.0%; Pred. No. 1,7e-102;

Matches 289; Conservative 75; Mismatches 165; Indels 16; Gaps 9;

OY 22 DYEDSPDTGVVRYTLLTEVDMMTGDPGVVKEKVMVNNSSITGPTFEADMGPTIOYTV 81

DB 46 DYENPTGTVTRKRLNLYVTEVDNIVGGDGLVKSAMLLNNQFPPIIKADMGDWEVTV 105

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QY 66 GPTLEADMGDTIQVTVINNNLETNGTSHHMGHLOKGNLHDGANGITECPKPKGRKY 125
D 2 GPTLEADMGDMIOVTLKNSMMPDNGTGHMGHLOKGNLHDGANGITECPKPKGRKY 60
QY 126 RFKAQOYGTSMYHSHFSAOYNGVGAIOINGPASPDPDTDGVPPISYSSADELVE 185
D 61 TFOATQFGTSMYHSHFSAOYNGVGAIOINGPASPDPDTDGVPPISYSSADELVE 120
QY 186 LTKNS--CAPESDNYLFGNTAKHP--ETGESEYANVTLPGRHRLRLINTSEVNHFOYS 241
D 121 RIASHQAPRPSDNDGLNGSMAPAGQTC--GKTTNTITAGKKYRLRLINTSEVNHFOYS 179
QY 242 LVNHTMCIADMPVNAFVDSLFVGYGQRYDVIANRPTGNTFVNTFGGLCG-G 300
D 180 LDNHAFTVTSDFVIVETATNMIFIGORRYDVILTANQTVGSYWFRAEVONG--CGTN 237
QY 301 SRNPRAIIFHAGAPRPPDEGKAPVDHNCLEPRLKPVYARV---PLSGFAKRAKN 357
D 238 NNNNGIKSIFETYSGAASPTSSA--TPYTGCTDEGTIIPWDSFVPSGSLSGNVEQLNV 296
QY 358 TLDVLTDTGTFPLFWKNGSAINIDMGRAVDYVLTONTSEPPGYIYEANGADQMSY 417
D 297 AINIGVDASG--PIYTWGINSALIDVDMKPIQYVLDGNSMPASENLELEPNAQWY 355
QY 418 LIENDPG-----APFTLPHPMHLGHDFYVLSGRSPDESASNERHVEDPARDAGLSGA 471
D 356 VIOEYVGNVGNPVSINVPHPMLHGHDFELG---TCVGTYNNTINGPSLDYD----- 406
QY 472 NPVRDYSMLPFGWVYLSFRADNPGAMLFHCHIAMHVSGLGVY 517
D 407 NPTRDVAMLPAGMWVLAFTDNGPAMLMHCHIAMHVSGLGVY 452

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## RESULT 4

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QY 096WM9 PRELIMINARY; PRT: 581 AA.
AC 096WM9;
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
DE Laccase 2 (EC 1.10.3.2).
GN LCC2.
OS Botrytis cinerea (Botryotinia fuckelliana).
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Leotiomycetes;
OC Helotiales; Sclerotiniaceae; Botryotinia.
OX NCBI_TaxID=40559;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=SA556;
RA Schouten A., Vermeer J.E.M., van Kan J.A.L.;
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF243855; AAK77953.1;
DR InterPro: IPR001117; Cu-oxidase.
DR InterPro: IPR002355; Multicu_oxidase2.
DR Pfam; PF00394; Cu-oxidase; 3.
DR PROSITE; PS00079; MULTICOOPER_OXIDASE1; UNKNOWN_1.
DR PROSITE; PS00080; MULTICOOPER_OXIDASE2; UNKNOWN_1.
KW Oxidoreductase.
SQ SEQUENCE 581 AA: 63434 MW: 674947DAFD6BC757 CRC64;

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Query Match 33.9%; Score 1071.5; DB 3; Length 581;  
 Best Local Similarity 38.4%; Pred. No. 1.2e-69;  
 Matches 220; Conservative 103; Mismatches 205; Indels 45; Gaps 17;

```

QY 3 SC-NTPSNRACGTGDTQVTVINNNLETNGTSHHMGHLOKGNLHDGANGITECPKPKG 60
D 38 SCANSAITSKSCGE--YSDTNNYDVPTGVTREYTWLS--VENSTTTPDGTYR--SAMTF 92
QY 61 NNSIGPTIFADMGDTIQVTVINNNLETNGTSHHMGHLOKGNLHDGANGITECPKPKG 120
D 93 NOTVGPATITADMGDMNLIIHYTNNLQHNCTSHHMGHLOKGNLHDGANGITECPKPKG 151

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QY 121 GRRVYRFKAQOYGTSMYHSHFSAOYNGVGAIOINGPASPDPDTDGVPPISDYSSA 180
D 152 DLTGFKFOATQYGTSMYHSHFSLOVADGLEPPLINGPATADVEDVGAIFLQDMHRSY 211
QY 181 DELVELTKNSGAPESDNVLEFNGTAKHP-----GGESEYANVTLPGRHRLRLINT 232
D 212 FEIMDSARQAGAPPALENTLMTNGTINIDCSASTDANCVGGRKFELEFVECTKRLRLIN 271
QY 233 SEVNHFOYSLVNHTMCIADMPVNAFVDSLFVGYGQRYDVIANRPTGNTFVNTFG 292
D 272 GIDSHFEFRIIDNHTLVIANDLPIYPTDTLLIGIRYDVIANNAADWYRLRGW 331
QY 293 GGLCGGSRNPYA-AIFHYAGAPRPPDEGKAPVDHNCLEP--NLKPVYARVPLVS 349
D 332 --GTCSSNSEAMATGILRYDSSYVDPSTVGTPE--RGTCADEPYASLVPPLHALDV--G 386
QY 350 GFKAADRNTLDTDTGTFPLFWKNGSAINIDMGRAVDYVLTONTSEPPGYIYEANG 409
D 387 GT-----SLVDEQVSPAFNTFTWTNSSLIDMSSPTTLKIFENNETTIPDYVVALN 441
QY 410 GAD--QMSYWLIENTDPGAPFTLPHPMHLGHDFYVLSGRSPDESASNERHVEDPARDAG 466
D 442 QIDANEWVYVYIEDLTG--FGIMHPILHGHDFYVVADET-----VESATKPSA 490
QY 467 LLSGANPVRRDYSMLPFGWVYLSFRADNPGAMLFHCHIAMHVSGLGVYLERADDLRG 526
D 491 NFNLVPPRPDVAALPGNGCYLAIFELKIDNPGSWLLCHIAMHVSGLGVYFVESQSSI-- 548
QY 527 AVSDADADDLDRICADMRRTYPTNPYKSDGL 559
D 549 ALGMSDTLFDTCANMNAITPELFAEDDSGI 581

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## RESULT 5

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QY 096WM9 PRELIMINARY; PRT: 561 AA.
AC 096WM9;
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
DE Laccase 1 (EC 1.10.3.2).
GN LCC1.
OS Botrytis cinerea (Botryotinia fuckelliana).
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Leotiomycetes;
OC Helotiales; Sclerotiniaceae; Botryotinia.
OX NCBI_TaxID=40559;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=SA556;
RA Schouten A., Vermeer J.E.M., van Kan J.A.L.;
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF243854; AAK77952.1;
DR InterPro: IPR001117; Cu-oxidase.
DR InterPro: IPR002355; Multicu_oxidase2.
DR Pfam; PF00394; Cu-oxidase; 3.
DR PROSITE; PS00079; MULTICOOPER_OXIDASE1; UNKNOWN_1.
DR PROSITE; PS00080; MULTICOOPER_OXIDASE2; UNKNOWN_1.
KW Oxidoreductase.
SQ SEQUENCE 561 AA: 60336 MW: 7F36B8289EF73C23 CRC64;

```

Query Match 30.9%; Score 974.5; DB 3; Length 561;  
 Best Local Similarity 36.9%; Pred. No. 1.2e-62;  
 Matches 209; Conservative 82; Mismatches 229; Indels 47; Gaps 15;

```

QY 1 QOSC-NTPSNRACGTGDTQVTVINNNLETNGTSHHMGHLOKGNLHDGANGITECPKPKG 56
D 34 ROSCANATATRSKCGO--YASASTSYTYVTKGTGLVLYVONTLS-----ADG--VSRP 82
QY 57 VMLVNSIIGPTIFADMGDTIQVTVINNNLETNGTSHHMGHLOKGNLHDGANGITECPKPKG 116
D 83 TLNFGNCTIGPQTADMGDDVIVHTNKLTSNGTSHHMGHLOKGNLHDGANGITECPKPKG 142
QY 117 PRGGRKYVRFKAQOYGTSMYHSHFSAOYNGVGAIOINGPASPDPDTDGVPPISDY 176

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OY 125 YRFKAOQGTSMYSHSFAOYGNQGVAGIQLNGPASI,LPYFDLGGVPSIOYYSASDELV 184
Db 165 YKFRYTOYGTWYSHSFSLOJAEGLFGMFIYGTPTANDEJLSTLELODMDEGTAMHGW 224
OY 185 ELTRNSGA-PESDNYLENGT---AKHDE---TGEGEYANVTLLTGRHRRLRLIMTSVE 235
Db 225 DNVAASKGAGPLPANGLLIWTFTPOCKNSTDNCVGCGKKFSANPKKKKHLIRIINNSAD 284
OY 236 NHFOVSLNHNHCIIADMYVPMVNMATYDSLELGVOGRYDYVIEANKRPPGYWYENVTFGG 285
Db 285 AHFOESIDGDLFYVAVNDLVPIKPKFKTSYVSGORYDVAIVENAPRGWYMLR---SG 340
OY 296 LLC-----GGSNRPYPAIFHTAGAPGCPTEDEGKAPVDHCL--DEPNLRKPVANRPLS 349
Db 341 MSCVPDGGALRKRYVTGIIRDKKSKADPKTTSOVVYDEFCSDSDPKKVLPHLALDVTHT 400
OY 330 GFAPKADNTLDVYTLDTTGTPL-----FYWKYNSGAINIDMGRAVYDYVLTQNTSEPPGYN 404
Db 401 GEIYRS---DLGFRKPNGTPAEGONWFQWLTNNSSLVIMDHPLERLIFGOSJFFPYDYN 456
OY 405 IVEVNGADONSTWML-----ENDPGAPFTLLPPIHLHGDFVILGRSP---DESP 451
Db 457 YIKAD-CQLMWQAMVHTGSEQRPDPDLPSHNLAPRIHLHGDFVWLSQSKAKWDGTP 515
OY 452 ASNERHVEFDPARADGGLSGANPVRBDVSMLEPAFGVYVLSFRANDPGAMLEFHCIIAMHVS 511
Db 516 RG-----FDT-----KNPARDRDTAMLEPEKSHILAIQOLDNPGAMLVNHCIIAMHAG 561
OY 512 GLGVVYLERADLDGAVSDADADDLRLCADMKRYKTYPTNYPKSDSL 559
Db 562 GLSLSEFVSOD--RIALGMPNHVDVFRQTCREKMDVKTMPKPSDGI 607

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	RESULT	8			
Q8TFD9	ID	Q8TFD9	PRELIMINARY;	PRT;	578 AA.
AC	Q8TFD9;				
DT	01-JUN-2002	(TREMBLrel, 21, Created)			
DT	01-JUN-2002	(TREMBLrel, 21, Last sequence update)			
DE	01-JUN-2002	(TREMBLrel, 21, Last annotation update)			
GN	Laccase precursor (EC 1.10.3.2).				
OS	Gaeumannomyces graminis var. graminis.				
OC	Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;				
OX	Sordariomycetes incertae sedis; Magnaporthaceae; Gaeumannomyces.				
RN	NCBI_TaxID=36780;				
RP	[1]				
RA	SEQUENCE FROM N.A.				
RL	Litvinitseva A.P.;				
RT	"Genetics of laccase in Gaeumannomyces graminis, the take-all fungus.";				
RL	Thesis (2002), Department of Microbiology,				
RL	Montana State University -Bozeman, Bozeman, USA.				
DR	EMBL; AJ437320; CAD24842.1; .				
KW	Signal; Oxidoreductase.				
FT	SIGNAL	1	15	POTENTIAL.	
FT	CHAIN	16	578	POTENTIAL.	
SO	SEQUENCE	578 AA;	63650 MW;	1A87EFA28742BD9C CRC64;	
	Query Match	29.8%;	Score 940.5;	DB 3;	Length 578;
	Best Local Similarity	36.0%;	Pred. No. 3.9e-60;		
	Matches 205;	Conservative 103;	Mismatches 215;	Indels 47;	Gaps 21.
OY	5	NTPSNRACATGTCGYDINTDEV--DSPTGTGVRRYYTLTLEVDNMNTGGDGVYKKEKMLVNNS	63		
Db	41	MTATRSQMCD-FDIKSDYDTGOHPPTGTRFMELETLSVK-LAGDGVR-YVQAENGT	97		
OY	64	IIGPITFDMDGCITGYTVYNLT--ENGTSIHMHGHKGKTNLHDGANGTECPPIPKGG	121		
Db	98	VGPFLIWMDDGDVVYIHTVTKLTQSINGSVNRHGHGKHQDYILSDSIVSVTYQCSPVP-GT	156		
OY	122	KRYVRFKAQQYCTSMWHSHFSADQYGNGVGVAIQINCPASLPYTDGLGVPISIDSYSSAD	181		

```

Db      : : : : : | | : | | | | | | | | | | | | | | | | | | | | : : : : : |
157  TQTKFKATNGSSMYHSHFLQAMQGVFPBGIIINGPASANTYEDYGMVVLSDMGKHTPD 216

Qy      182  ELVELTKNSGAPSDNVLNFGTAKHPETGE--GETANVTLPGRHRRLRLINTSVENHQ 239
      | | : : : | | : | | | | | | | | | | | | | | | | | | | | : : : : : |
Db      217  ELMHQAESQGPTELLNALINGMNVYGAEGNQTGRMETSEACKSYKFRIVNTAIDTHFK 276

Qy      240  VSLVNHIMCIADANVNVNMYATDSLEFLYGQGRDVIYEANR--TGQNTYFNTFBGGLL 297
      | | : : : | | : | | | | | | | | | | | | | | | | | | | | : : : : : |
Db      277  FGIHNHTLVYIALDFEVEPEYETTMVINGORVDYIVKDAQAVASDSEFLRAIPOSA-- 334

Qy      298  CGG---SRNPYPALIFHYACGPGPPNDEKAPVDNHCILP--NLKPYVARBPVLSGFA 352
      | | : : : | | | | | | | | | | | | | | | | | | | | | | | : : : : : |
Db      335  CGTLEMANN--TRAIYHIGNSQGVPEST--TGHTTYVD--ACEDEPLEKLPILIRIDAEOSTY 389

Qy      353  KRAANTLDVTLDITGTGTLFLVWKVGSANINIDGRVAVDYVLTONT--SEPPGYNIVEVNGA 411
      | | : : : | | : | | | | | | | | | | | | | | | | | | | | : : : : : |
Db      390  ---EQKATATGANGVNGVFRKRYLINSTMEIDMSNPYTSQLASNATVAFSSNMYMELPEA 446

Qy      412  DQMSYWLIEENDPGAFETLPHRPHMLHGDFYVLGSRPDESPASNERHVEPDARDAGLISGA 471
      | | : : : | | : | | | | | | | | | | | | | | | | | | | | : : : : : |
Db      447  DKMAYVITOTD---FGVAYILHGHGDSYVLAQSGS-----AYQCG--VTKLITT 491

Qy      472  NPVRRDYSMLPACFWYVLSFPAADNPGAMLFRCHTAMVYSGGLGVYVYLERDDL--KCAVS 529
      | | : | | : | | : | | | | | | | | | | | | | | | | | | | | : : : : : |
Db      492  NPMRRDPALEPAACHLVLAFTKDPBGMILMHCHIGWHTAAGFAMQFEVERSEMEFSKJIN 551
      | | : | | : | | : | | | | | | | | | | | | | | | | | | | | : : : : : |

Qy      530  DADADDIDRLCADRRRWYPTNPYKSSGL 559
      | | : : : | | : | | | | | | | | | | | | | | | | | | | | : : : : : |
Db      552  N---: : : : | | : : : | | : | | | | | | | | | | | | | | | | : : : : : |
552  N---NDIEGLCEPWRTHVGKINIKLESGI 578

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[illegible]



DT 01-JUN-2002 (Tremblrel. 21, last sequence update)  
DT 01-JUN-2002 (Tremblrel. 21, last annotation update)  
DE Laccase III (EC 1.10.3.2).  
OS Trametes versicolor (White-rot fungus).  
OC Eukaryota; Fungi; Basidiomycota; Hymenomycetes; Homobasidiomycetes;  
OC Aphyllophorales; Trametes.  
OX NCBI\_TaxID=5325;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Schuren F.H.J., Friesenegger A., Hessing J.G.M., Schneider C.,  
RA van Mulijik G.M., Dezan M., van Zeyl C.M.J.,  
RA van den Hondel C.A.M.J., Pfaller R.,  
RT "Laccase production by genetic transformation of the basidiomycete  
RT Trametes versicolor".  
RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.  
DR EMBL: AY081188; AAL93622.1; -.  
KW Oxidoreductase.  
SQ SEQUENCE 520 AA; 55473 MW; E1147EC32317C632 CRC64;

Query Match 20.1%; Score 636; DB 3; Length 520;  
Best local Similarity 33.0%; Pred. No. 4.7e-38;

Matches 183; Conservative 70; Mismatches 207; Indels 94; Gaps 23;

QY 31 GVRPTTLTLEVDNMTGPGVYKEMLVNNSITGPTIFADMGDTIQVYINNLETN-- 88  
DB 24 GPVADLTITNAAV---SPDGFSSROAV-VVNGGTPPLITGMDRFLANVINDLNTNHTM 78  
QY 89 -GTSIHMHGKHOKGTLHOGANGITECPIPKGRKRYRPKA-QOYGTWYSHSFAOY 145  
DB 79 LKSTISHMHGFFQKGTWMDGPAFINOCPI-SSGHSFLIDPQVDPQAGTFWHSLSYX 137  
QY 146 GNGVGAIOI---NGPASPYPDTDLG--VPEPIDYVYSSADELVELTKNSGAPF---SDN 197  
DB 138 CCGLRGFEVYDPRDPAADYDVNDPVTITLADWYHVA-----KLGPAPPLGADA 189  
QY 198 VLENGTAKHEGTGEAYANTLTGRRRLRLINTSVENHFQVSLVNHHTCIIADMYPV 257  
DB 190 TLINGKGRSPSTTADLTIVISVTPGKRYRFLVLSICDPNHTFSIDGNMTIIEFDSINT 249  
QY 258 NAMTVDSLFLVGCGORYVYVEANRTPGNYMF--NVTFGGGLGSGSRNPYPALIFHYGA 315  
DB 250 APLVVDSTIQIPAAORISFVLEANOAVNYMIRANPSFGNGFTGIN---SAILRIDGA 305  
QY 316 PGGPPTDEGRAPVDHNCIDLPNLEKPVYARVPLSGFAKRADNTLDVLTGTPLFYWKV 375  
DB 306 AALEPTTQTSTEP--LNEVNLHLIVATVPGSPVAGVDLATNMAFNENGTNPF--I 360  
QY 376 NSAINIDMGRAVVDYVL-TQNTS--FPPG--YNIIVEYNGADQWSYWLIENTDPCAPFTLP 430  
DB 361 NGASFPTPTVPLVLIQIISGAQNOADLLPSGSVSLPS-NADIEISFPATAAPGA---P 415  
QY 431 HPMHLHGHDFFYVLRSPDESPASNERHVFDPADAG--ILSGANPVRRDY--SMULPAFG- 485  
DB 416 HPFHLHGHAFAVY-----KSGSTVYINYNPIFRDYVSTGTPAAGD 456  
QY 486 WYVLSFRADNPGAWLFRCHIAHMYSGSLGVYLLERADLRGAVSDADADDRLCADWRR 545  
DB 457 NYTIRFRTDNPWFHLCHIDFHLFAGRAVYFAADIPDVASA----- 498  
QY 546 YWPTNPTPKSDSGL 559  
DB 499 ----NPVQAAMSDL 508

Search completed: December 4, 2002, 10:47:41  
Job time : 42 secs

GN CVL3.  
OS Coriolus versicolor.  
OC Eukaryota; Fungi; Basidiomycota; Hymenomycetes; Homobasidiomycetes;  
OC Aphyllophorales; Coriolus.  
OX NCBL\_TaxID=57466;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN-IF030340;  
RA Mikuni J.;  
RL Submitted (OCT-1992) to the EMBL/GenBank/DBJ databases.  
RN [2]  
RP SEQUENCE FROM N.A.  
RC STRAIN-IF030340;  
RA Iimura Y.;  
RL Submitted (SEP-1997) to the EMBL/GenBank/DBJ databases.  
DR EMBL: D13372; BAA22153.1; -  
DR InterPro: IPR001117; Cu-oxidase.  
DR Pfam: PF00394; Cu-oxidase; 3.  
DR PROSITE: PS00079; MULTICOPPER\_OXIDASE1. 1.  
KW Oxidoreductase; Signal.  
FT SIGNAL 1 21  
SQ SEQUENCE 520 AA; 55528 MW; F99429EAC9D71B0 CRC64;

Query Match 20.4%; Score 645; DB 3; Length 520;  
Best Local Similarity 33.2%; Pred. No. 1e-38;  
Matches 184; Conservative 70; Mismatches 206; Indels 94; Gaps 23;

QY 31 GVVAPYTLTLEVDNMTGPDGVVKEKVMVNSIIGPTIFADMGDTIQVTVINNLETN-- 88  
DB 24 GPVADLTITNAAV-----SPGFSRQAV-VVNGGTPGLITGNMGRQANVINDLTHHTM 78  
QY 89 --GTSIMHGLHOKGTLHMGANGITECPIPPKGKRVYEFKA-QQYGTSTHSHFSQY 145  
DB 79 LKSTSIHMHGEPFGKGMADGPAPINOCPI-SSGHSFLYFQVDPDAGTFYHSHLSTQY 137  
QY 146 GNGVGAIOI---NGPASPFDYDLG--VPEISDYSSADELVELTKNSGAPF---SDN 197  
DB 138 CDGLRGPFVYDPRPADLDYDNDOTVITLVDWYHVA-----KIGPAPFLGADA 189  
QY 198 VLENGTAKHPEETGEGEYANVTLPGRRRRLRLINTSVENHFOVSLVNHHTMCIIAADVPV 257  
DB 190 TLINGKRSPTTADLSVTSVTPGKRYRFLVSLSCDPNTFTSIDGHNTIETDSINT 249  
QY 258 NAMTVDSLEFVGGRYDVYIEANRTPGNYF--NVTGGGLCGGSRNPFAALFHYAGA 315  
DB 250 APLVVDLSIQIFPAORISFYLEANQAVDNTYIRANPNNGNGFTGIN---SAILRYDGA 305  
QY 316 PGGPPTDEGKAPVDHNCIDLPNLKPVVARDVPLSGFAKRAADNTLDVTLDTGTPLFV 375  
DB 306 AAVEPTTQTTSTP-----LNEVNLHPVATVAPGSPVAGVDLAINMAFNNGTNF-- 360  
QY 376 NSAINIDMGRAVVDYVL-TQNTS--PPEG--YNIYEVGADQMSYLIENDGAPFTLP 430  
DB 361 NGASFPTPTVYLLQIISGAQMODLLPSGSVYSLPS-NADIEISFPTAAAGA---P 445  
QY 431 HPHMLHGHDYVLRSPDESDESPASNERHYFDPADAG--ILSGANPYRVDY--SMLPAFG- 485  
DB 416 HPHHGHAFV-----RSAGSTVYNDPIFRDVSSTGTPAAG 436  
QY 486 WVYLSFRADNRGAMLFCHIAMHVSGLGVYLLERADDLRGAVSDADADDRLCADMR 545  
DB 457 NVYIRFTDNDPGPFLCHIDFHLGFAVFAEDIDPVASA----- 498  
QY 546 WYPTNPYKSDSGL 559  
DB 499 -----NPVQAWSDL 508

RESULT 14  
ID 096UT7 PRELIMINARY; PRT; 520 AA.  
AC 096UT7;  
DT 01-DEC-2001 (TReMBLrel. 19, Created)

DT 01-DEC-2001 (TReMBLrel. 19, Last sequence update)  
DT 01-MAR-2002 (TReMBLrel. 20, Last annotation update)  
DE Laccase B precursor (EC 1.10.3.2).  
GN LAC1.  
OS Trametes versicolor (White-rot fungus).  
OC Eukaryota; Fungi; Basidiomycota; Hymenomycetes; Homobasidiomycetes;  
OC Aphyllophorales; Trametes.  
OX NCBL\_TaxID=5325;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN-ATCC 32745;  
RA Jolivalt C., Madzak C., Caminade E., Mougin C.;  
RT "2,5-xylydine induced laccase from the basidiomycete Trametes versicolor ATCC 32745."  
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.  
DR EMBL: AF414109; AL07440.1; -  
DR InterPro: IPR001117; Cu-oxidase.  
DR Pfam: PF00394; Cu-oxidase; 3.  
DR PROSITE: PS00079; MULTICOPPER\_OXIDASE1. UNKNOWN\_1.  
KW Oxidoreductase; Signal.  
FT SIGNAL 1 21  
SQ SEQUENCE 520 AA; 55576 MW; F3241CB929C247F9 CRC64;

Query Match 20.3%; Score 640; DB 3; Length 520;  
Best Local Similarity 33.2%; Pred. No. 2.4e-38;  
Matches 185; Conservative 69; Mismatches 203; Indels 100; Gaps 24;

QY 31 GVVAPYTLTLEVDNMTGPDGVVKEKVMVNSIIGPTIFADMGDTIQVTVINNLETN-- 88  
DB 24 GPVADLTITNAAV-----SPGFSRQAV-VVNGGTPGLITGNMGRQANVINDLTHHTM 78  
QY 89 --GTSIMHGLHOKGTLHMGANGITECPIPPKGKRVYEFKA-QQYGTSTHSHFSQY 145  
DB 79 LKSTSIHMHGEPFGKGMADGPAPINOCPI-SSGHSFLYFQVDPDAGTFYHSHLSTQY 137  
QY 146 GNGVGAIOI---NGPASPFDYDLG--VPEISDYSSADELVELTKNSGAPF---SDN 197  
DB 138 CDGLRGPFVYDPRPADLDYDNDOTVITLVDWYHVA-----KIGPAPFLGADA 189  
QY 198 VLENGTAKHPEETGEGEYANVTLPGRRRRLRLINTSVENHFOVSLVNHHTMCIIAADVPV 257  
DB 190 TLINGKRSPTTADLSVTSVTPGKRYRFLVSLSCDPNTFTSIDGHNTIETDSINT 249  
QY 258 NAMTVDSLEFVGGRYDVYIEANRTPGNYF--NVTGGGLCGGSRNPFAALFHYAGA 315  
DB 250 APLVVDLSIQIFPAORISFYLEANQAVDNTYIRANPNNGNGFTGIN---SAILRYDGA 305  
QY 316 PGGPPT---DEGKAPVDHNCIDLPNLKPVVARDVPLSGFAKRAADNTLDVTLDTGTPLFV 372  
DB 306 AAVEPTTQTTSTP-----LNEVNLHPVATVAPGSPVAGVDLAINMAFNNGTNF-- 359  
QY 373 WYVNSAINIDMGRAVVDYVL-TQNTS--PPEG--YNIYEVGADQMSYLIENDGAPFTLP 427  
DB 360 --INGASFPTPTVYLLQIISGAQMODLLPSGSVYSLPS-NADIEISFPTAAAGA-- 414  
QY 428 TLPHMLHGHDYVLRSPDESDESPASNERHYFDPADAG--ILSGANPYRVDY--SMLPA 483  
DB 415 --PHPEHGHAFV-----RSAGSTVYNDPIFRDVSSTGTPA 453  
QY 484 FG-WVYLSFRADNRGAMLFCHIAMHVSGLGVYLLERADDLRGAVSDADADDRLCAD 542  
DB 454 AGDNVTIRFTDNDPGPFLCHIDFHLGFAVFAEDIDPVASA----- 498  
QY 543 WYPTNPYKSDSGL 559  
DB 499 -----NPVQAWSDL 508

RESULT 15  
ID 08TFM1 PRELIMINARY; PRT; 520 AA.  
AC 08TFM1;  
DT 01-JUN-2002 (TReMBLrel. 21, Created)







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Db 143 AFGGTLTKFADNADGSSWYSHFLLQYGDGLFGLVINGPATFANVDGLFLINDNM 201
OY 177 YSSADELVELTNSGAPESDNLFNGTAKHPETGESEYANVTLPGRHRRLINTSVEN 236
Db 202 HVPVOSLMDKAKTGAFTLLTGLMNGTNY--NGACKFQJTFPTPGIKRIRVAVTAVDG 259
OY 223 HVOVSLVNTMCIADAMPVNAATVDSLFGVGRYDVYIEANRPNGYVNTVETGGGL 296
Db 260 HRFQSTIDGSHFOYIADFPVIVPYNATSLIVSTIAQRIDITVTAAGVNTW--IRAGMOT 317
OY 297 LCGSHNPP-ALIFHYAGAPG-GPPTDEGKAPVDHNCIDLPMIKPVYARVPLSGFAKR 354
Db 318 ACGSNMANNANIGILTKYTSSTSTADPTTSTVYASTSCDEP-----LALVFPVPIPV 372
OY 355 ADNTLDVTLDTGTPLFVKVNGSAINIDGRAVVDVYLTONTSPFGPIVYENGADOM 414
Db 373 ASSIMKTTLTGGGQ--MLFNSSLLMWTDEPLTLVINSGNIMPLEYVPIESTTAN 429
OY 415 STW--LIENDPGAPFTLPHMHLHGDFVYLGSRSPESASNERHVPDPARAGLLSGAN 472
Db 430 KMAVLAISGPNP--NHPIHLHGDFWTLSCGTGATYATP-----ALNLVN 474
OY 473 PVARDYSMLPARGWVYLSPRDNPGAMLPHCHIAHVSGLGVYLLERADLNGAVSDAD 532
Db 475 PPRROVWTLPTGSHLVIAFOIONPGSMLMCHIAHNSGELALQFVSESSILPTGTAD 534
OY 533 ADDDLRLCADMRIRYPTNPEPKSDSGI 559
Db 535 VSTFQNTCAAMKAWPTPEPPDDSGI 561

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## RESULT 6

08TFE4 PRELIMINARY: PRT: 608 AA.

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AC 08TFE4;
DT 01-JUN-2002 (TREMblrel. 21, Created)
DT 01-JUN-2002 (TREMblrel. 21, last sequence update)
DT 01-JUN-2002 (TREMblrel. 21, last annotation update)
DE Laccase precursor (EC 1.10.3.2).
GN LAC1.
OS Gaemannomyces graminis var. tritici.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC Sordariomycetes Incertae sedis; Magnaporthaceae; Gaemannomyces.
OX NCBI_TaxID-36779;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE-21861250; PubMed-11872481;
RA Litvinseva A.P.; Henson J.M.;
RT "Cloning, characterization, and transcription of three laccase genes
RT from Gaemannomyces graminis var. tritici, the take-all fungus.";
RL Appl. Environ. Microbiol. 68:1305-1311(2002).
RN [2]
RP SEQUENCE FROM N.A.
RA Litvinseva A.P.;
RT "Genetics of laccase in Gaemannomyces graminis, the Take-All
RT fungus.";
RL Thesis (2002), Department of Microbiology,
RL Montana State University-Bozeman, Bozeman, USA.
DR EMBL: AJ417685; CAD10747.1; -.
KW Signal; Oxidoreductase.
FT SIGNAL 1 18
FT CHAIN 1 18
SQ SEQUENCE 608 AA: 67421 MW: 094F7852FAA602F0 CRC64;

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Query Match 30.2%; Score 954; DB 3; Length 608;

Best Local Similarity 35.5%; Pred. No. 4.3e-61;

Matches 209; Conservative 94; Mismatches 223; Indels 62; Gaps 17;

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OY 5 NPSNRACWTDGYDINTDYVSDPVGVRPYTLTLEVDNMTGPDGVVEKVALVNNSTI 64
Db 50 NGRKSRNCW-GKSIDINNYETAPDGTREYMLSVBE--GICNNDG-YKRYCOTFNGSF 105
OY 65 IGPTIFADMGDTIOVYINNLKNGTISIHMHGLHQKGTNLHDGANGITECPDIPKGRKV 124

```

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Db 106 PGPLIANNMGDNLVIHYTNMKNKTNGTALIHMHGLHQGSVEYDGPVTCQPIAP-GKSLT 164
OY 125 YRFKAQOYGTSWYSHFSAOYNGVGAIOINGPASPILPTDGLVPISSDIYSSADELY 184
Db 165 YKFRVYQYGTWYSHFSLQYTGELGPMFYGPPTANVEDDGLTFLDMDHDTAMHNG 224
OY 185 ELKFNKA-PESDNLVFNCG--AKHPET--GGGEVANYTLTGRHRRLINTSVYE 235
Db 225 ENVASGAGPLPANGLINGNTFDCKNSTDTNCLGGGKSATFKKAKHLININNSD 284
OY 236 NHOVSLVNTMCIADAMPVNAATVDSLFGVGRYDVYIEANRPNGYVNTVETGGG 295
Db 285 AHRQFSTIDGSHLIVSNDLPIKFKTQSVRSVIGRQYDIVEANMKPGDYMLR--SG 340
OY 296 LLC--GGRNPPAALIFHYAGAPGPPDEKAPVDHNC--DLNPKPVYARVPLS 349
Db 341 MSCVPDGTGALRRRYVGIIRYDKSKADPKTSDVYVDETCSDEDPKRLPVHALDYTH 400
OY 350 GFAKRADNTLDVTLDTTGPPL--FVWKVNGSAINIDGRAVVDVYLTONTSPFGVN 404
Db 401 GEIVQS--DLGFKPNGTPABGQNMFOVTLNNSSLVDHDPPTLEKIPDROSIFPTKYN 456
OY 405 IVEVN--GADQWSYLIEND--PGAPFTLPHMHLHGDFVYLGSRP--DESP 451
Db 457 VIAEPATAPASKMFTLVIOSEILTLPLSHSLTRPHLHGDFWVLSQSAKMDGTP 516
OY 452 ASNERHVPDPARDAGLISGANPVARDYSMLPARGWVYLSPRDNPGAMLPHCHIAHVS 511
Db 517 RG-----FNTNPARBDYAMLPAAGHIALAFOJLNPGLMVLCHIAHMHAG 562
OY 512 GLGVYLLERADLNGAVSDADDDLRLCADMRIRYPTNPEPKSDSGI 559
Db 563 GLSEFVESQG--RIALGMPDHHVFOQTCREMDAVRRKMPFPQDSDGI 608

```

## RESULT 7

08TFE1 PRELIMINARY: PRT: 607 AA.

```

AC 08TFE1;
DT 01-JUN-2002 (TREMblrel. 21, Created)
DT 01-JUN-2002 (TREMblrel. 21, last sequence update)
DT 01-JUN-2002 (TREMblrel. 21, last annotation update)
DE Laccase precursor (EC 1.10.3.2).
GN LAC1.
OS Gaemannomyces graminis var. graminis.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC Sordariomycetes Incertae sedis; Magnaporthaceae; Gaemannomyces.
OX NCBI_TaxID-36780;
RN [1]
RP SEQUENCE FROM N.A.
RA Litvinseva A.P.;
RT "Genetics of laccase in Gaemannomyces graminis, the take-all
RT fungus.";
RL Thesis (2002), Department of Microbiology,
RL Montana State University-Bozeman, Bozeman, USA.
DR EMBL: AJ437319; CAD24841.1; -.
KW Signal; Oxidoreductase.
FT SIGNAL 1 18
FT CHAIN 19 607
FT SIGNAL 19 607
SQ SEQUENCE 607 AA: 67595 MW: 908C01BC3E2AD7F CRC64;

```

Query Match 30.2%; Score 953.5; DB 3; Length 607;

Best Local Similarity 35.9%; Pred. No. 4.7e-61;

Matches 211; Conservative 87; Mismatches 227; Indels 63; Gaps 18;

```

OY 5 NPSNRACWTDGYDINTDYVSDPVGVRPYTLTLEVDNMTGPDGVVEKVALVNNSTI 64
Db 50 NGRKSRNCW-GKSIDINNYETAPDGTREYMLSVBE--GICNNDG-YKRYCOTFNGSF 105
OY 65 IGPTIFADMGDTIOVYINNLKNGTISIHMHGLHQKGTNLHDGANGITECPDIPKGRKV 124
Db 106 PGPLIANNMGDNLVIHYTNMKNKTNGTISIHMHGLHQGSVEYDGPVTCQPIAP-GKSLT 164

```

OY 82 INNETSTSTIMHHLHOKGTNHLHGANGITIECPRLPPGKGRKRYKFRKQOXTSMYSHF 141  
 Db 106 TNRRLTNTSTMHMHGVRRLNNPNPDGANGITIECPRLPNAS-KYVRFRFQJGTAMYSHF 164  
 OY 142 SAOTGNGVYGAIIQINGPASPRLPYDDLGVPFISDYSSADEL-VELTNSGA-PPSDNVL 199  
 Db 165 SGOYNGVYGTLLFEGPASPRLPYOEDLGVPYPTDMWYRGADIEIOPSLIPSPVPPSDNVL 224  
 OY 200 FNGTAKHETEGEGEYANTLTTPGRHRRLRLINTSVENHFOYSIVNHMTCIIAADVVPNA 259  
 Db 225 FNGSHVNAQ-GGGSTNRVKLPRGRHRRLRLINTSVDNFTVSLGHQFTVLIQTDVFPNA 283  
 OY 260 MYVDSLFLVAGVGRYVYVEANRTPGNMYFNTFFGGGLGCGSRNFPAPAFHYAGAP-G 318  
 Db 284 FTTSGIFLIGIGORVDTLEAQPVGNDMFNTYFASGLCGTSLQKPAISIQYEGASDTA 343  
 OY 319 PPTDEGKAPVNDHCLDLENLKAPVARADYPLSGFAKRADNTLDYLT---TGTPLFWKV 375  
 Db 344 LPTNGPPTPSTSLCDLMSWTTPYAKNVPASFSFSAVPNTLEANTVENMGKORUYEI 403  
 OY 376 NGSANINMGRAVVDYVLTONTSPFGNYIYEVNADQMSWLIEINDGAPPTLPHMHL 435  
 Db 404 NCSDMNTIMTDEPTLETLYLKGNMNFQNNVQYVPGNOMSTRICTION----PTVAPHMHL 459  
 OY 436 HGHDFYVLGRSPDE-SPASNERHVPDPARDAGLLSGANPVRDYSMLPAFGVYVLSFRAD 494  
 Db 460 HGHDFYLLGRSPAQNPFPAGPYRRFNATDLATLRFDPNPRDVTMLPANGYIVAFPTD 519  
 OY 495 NPGALFPHCHIAHMYSGGVYLLERADDLRGAVSDADADDLRLCAOMRRYMPNPPK 554  
 Db 520 NPGALFPHCHIAHMYAOGLSVQFLERVDIPSAF---PLSAIEPTCSOMTAYATISPKQ 576  
 OY 555 SDSGL 559  
 Db 577 HDSGL 581  
  
 RESULT 2  
 O9C497 PRELIMINARY: PRT: 589 AA.  
 ID O9C497  
 AC O9C497:  
 DT 01-JUN-2001 (TREMBLrel. 17, Created)  
 DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)  
 DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)  
 DE Lacase.  
 GN LACI.  
 OS Glomerella lagenarium (Anthracnose fungus) (Colletotrichum lagenarium).  
 OS Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes; Sordariomycetes incertae sedis; Phyllachorales; Phyllachoraceae; mitosporic Phyllachoraceae; Colletotrichum.  
 OC NCBI\_taxid=5462;  
 OX [1]  
 RN SEQUENCE FROM N.A.  
 RP STRAIN=104-T.  
 RC Tsui G., Fujikawa J., Ishida H., Horino O., Kubo Y.,  
 RA "Laccase gene laci of Colletotrichum lagenarium is not essential for melanin biosynthesis and pathogenicity".  
 RL Submitted (Feb-2001) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: AB055709; BAB32575.1; -.  
 DR InterPro: IPR001117; Cu-oxidase.  
 DR InterPro: IPR002355; MultiCu\_oxidase2.  
 DR InterPro: IPR001854; Ribosomal\_L29.  
 DR Pfam: PF00394; Cu-oxidase; 3.  
 DR PROSITE: PS00079; MULTICOOPER\_OXIDASE1; 1.  
 DR PROSITE: PS00080; MULTICOOPER\_OXIDASE2; 1.  
 DR PROSITE: PS00579; RIBOSOMAL\_L29; UNKNOWN.1.  
 SQ SEQUENCE 589 AA: 64652 MW: B206924563F8BE1 CRC64:

Query Match	46.3%;	Score 1461.5;	DB 3;	Length 589;
Best Local Similarity	50.3%;	Pred. No. 5e-98;		
Matches 285;	Conservative 84;	Mismatches 175;	Indels 23;	Gaps 13;

```

0Y      3 SCNT--PENRACMTDGDXYINDINDEVDSDTECVAPRTLLTLEVDNMTKPGGVAEKMLV 60
      1 1 1 : : : : : 1 1 1 : : : : : 1 1 1 : : : : : 1 1 1 : : : : :
Db      36 SCGHGPRPNRACMGMDININDYETSLPSTGQTVDFITTNVDFAA-DEISK-PRMLI 93
      1 1 1 : : : : : 1 1 1 : : : : : 1 1 1 : : : : : 1 1 1 : : : : :
0Y      61 NNSIGPTIEADMGDTQIVTVINNLETNGTSHHNGHLHOKGTMLHDGANGITECPRPKG 120
      1 1 1 1 1 1 1 : : : 1 1 1 1 1 1 1 : : : 1 1 1 1 1 1 1 : : :
Db      94 NGQFGPPTIEADMGDMVEINHNQDLADNGTSHHNGHNRNSNDQDANGVTECPPIAF-G 152
      1 1 1 1 1 1 1 : : : 1 1 1 1 1 1 1 : : : 1 1 1 1 1 1 1 : : :
0Y      121 GRKYRFEAAQOYGTSMNHSHESAQYGMGVGALQINGPASTPYTDLGVPPISDYTYSSA 160
      1 1 1 : : : : : 1 1 1 1 1 1 1 : : : : : 1 1 1 : : : : : 1 1 1 : : :
Db      153 HSKTKFEMIDYGTSMWHSHPSSQYGMGVGALKINGPASADYDIDLGPTVSDMYDTA 212
      1 1 1 : : : : : 1 1 1 1 1 1 1 : : : : : 1 1 1 : : : : : 1 1 1 : : :
0Y      161 DEL---VELTFKNSGAPFSDNVLFGTKAKHPTGSGEYANTLPGRHRRLINTFSEVN 237
      1 1 1 : : : : : 1 1 1 : : : : : 1 1 1 : : : : : 1 1 1 : : :
Db      213 DRLERQALVLNAGPPDSDNVLFGTNGTINMAO-GGGQYSKTKLPFGKKHRLINTPVDNT 271
      1 1 1 : : : : : 1 1 1 : : : : : 1 1 1 : : : : : 1 1 1 : : :
0Y      238 FOVSLVNTTMCILIADAMPVNAKMYVDLSLFLGQGRYVNVLEANKTPMYNFNTFGGGL 297
      1 1 1 1 1 : : : 1 1 1 : : : 1 1 1 : : : 1 1 1 : : : 1 1 1 : : :
Db      272 FTVSLVNGHSFVIATDYLPAKPVYKDSLFIIVGGRDYITIEADQVGNMYNMTLASGL 331
      1 1 1 : : : : : 1 1 1 : : : : : 1 1 1 : : : : : 1 1 1 : : :
0Y      298 CGGSFNRPYPAALFHYAGAPGPRPDEGKAPVDHNCOLD.PMLKPYAVADVPLSGFAKADN 357
      1 1 1 : : : : : 1 1 1 : : : : : 1 1 1 : : : : : 1 1 1 : : :
Db      332 CGTNAKPRPASIFTEGADLEPTEQGVPA-ADCVPTGTSPYLAAHAEAEETPN-KN 369
      1 1 1 : : : : : 1 1 1 : : : : : 1 1 1 : : : : : 1 1 1 : : :
0Y      358 TLDVLDOTT---GFLFPMXKXGSAININDMCRAYVDVLYONTSFPPGYNIVENGNDOM 414
      1 1 1 : : : : : 1 1 1 : : : : : 1 1 1 : : : : : 1 1 1 : : :
Db      390 ILDVLEDPETIHGEKIFHYMRWNGSSMDQOMKPLTQYTLAEGNSDMPQAHANVLESGADV 449
      1 1 1 : : : : : 1 1 1 : : : : : 1 1 1 : : : : : 1 1 1 : : :
0Y      415 SWYLENDPGAFETLPBPHMLHGDFYVLGRSPESPASNERHFDPDARDAGL--LSEGAN 472
      1 1 1 : : : : : 1 1 1 : : : : : 1 1 1 : : : : : 1 1 1 : : :
Db      450 TMMVYEN-TGA---LPRHILHGHDFLLGLGDGRKFSNSSSTNGTGYSSVKKYPSLAFAN 505
      1 1 1 : : : : : 1 1 1 : : : : : 1 1 1 : : : : : 1 1 1 : : :
0Y      473 PYVRDYSMLPAFGVVVLSFPAADPGAWLHFCHIAHVSGLGVYVLEPADLRGANSAD 522
      1 1 1 1 1 : : : 1 1 1 1 1 1 1 : : : 1 1 1 1 1 : : : 1 1 1 : : :
Db      506 PFRBDVAOLLPGGMVYAFETDTNPGAWMLHCHIAHVSMSLGYOFIERKEITLSALK--- 562
      1 1 1 : : : : : 1 1 1 : : : : : 1 1 1 : : : : : 1 1 1 : : :
0Y      533 ADDILRLCADNRRYPTNPYKPSGSL 559
      1 1 1 : : : : : 1 1 1 : : : : : 1 1 1 : : : : : 1 1 1 : : :
Db      563 LETLDQTCYMWKDYAHAAFPKYSGL 589
      1 1 1 : : : : : 1 1 1 : : : : : 1 1 1 : : : : : 1 1 1 : : :

```

```

RESULT 3
096UM2
ID 096UM2 PRELIMINARY: PRT: 454 AA.
AC 096UM2:
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
DE lacase (EC 1.10.3.2) (Fragment).
GN
OS Botrytis cinerea (Botryotinia fuckeliana).
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Leotiomycetes;
OC Helotiales; Sclerotiniaceae; Botryotinia.
OX NCBI_TaxID=40559;
RN [1]
RP
RP SEQUENCE FROM N.A.
RA Schouten A., Deloy S., van Kan J.A.L.;
RL Submitted (JUL-2001) to the EMBL/Genbank/DBJ databases.
RL EMBL: AY047482; AAL06114.1; -.
DR InterPro: IPR001117; Cu-oxidase.
DR InterPro: IPR002355; MulticCu-oxidse2.
DR Pfam: PF00394; Cu-oxidase; 3.
DR PROSITE: PS00079; MULTICOPPER_OXIDASE1; UNKNOWN_1.
DR PROSITE: PS00080; MULTICOPPER_OXIDASE2; UNKNOWN_1.
KW Oxidoreductase.
KW
KW FT NON_TER 1
KW FT NON_TER 454
KW SEQUENCE 454 AA; EB56A720394D912A CRC64;

Query Match 35.3%; Score 1113.5; DB 3; Length 454;
Best Local Similarity 47.2%; Pred. No.7.2e-73;
Matches 220; Conservative 72; Mismatches 145; Indels 29; Gaps 12;

```

**Gaps** 12;

DR InterPro: IPR002355; MultiCu\_oxidase2.  
 DR Pfam: PF00394; Cu-oxidase; 3.  
 DR PROSITE: PS00079; MULTICOPPER OXIDASE1; FALSE\_NEG.  
 DR PROSITE: PS00080; MULTICOPPER OXIDASE2; FALSE\_NEG.  
 KM Oxidoreductase: Signal; Copper; Metal-binding; Glycoprotein; Repeat;  
 KW Lignin degradation; Multigene family; Polymorphism.

FT SIGNAL 1 19  
 FT CHAIN 20 531 LACASE 4.  
 FT DOMAIN 23 146 PLASTOCYANIN-LIKE 1.  
 FT DOMAIN 158 315 PLASTOCYANIN-LIKE 2.  
 FT DOMAIN 384 507 PLASTOCYANIN-LIKE 3.  
 FT METAL 83 83 COPPER (TYPE 2) (BY SIMILARITY).  
 FT METAL 85 85 COPPER (TYPE 3) (BY SIMILARITY).  
 FT METAL 128 128 COPPER (TYPE 3) (BY SIMILARITY).  
 FT METAL 130 130 COPPER (TYPE 3) (BY SIMILARITY).  
 FT METAL 427 427 COPPER (TYPE 1) (BY SIMILARITY).  
 FT METAL 430 430 COPPER (TYPE 2) (BY SIMILARITY).  
 FT METAL 432 432 COPPER (TYPE 3) (BY SIMILARITY).  
 FT METAL 479 479 COPPER (TYPE 3) (BY SIMILARITY).  
 FT METAL 480 480 COPPER (TYPE 1) (BY SIMILARITY).  
 FT METAL 481 481 COPPER (TYPE 3) (BY SIMILARITY).  
 FT METAL 484 484 COPPER (TYPE 1) (BY SIMILARITY).  
 FT METAL 2 2 COPPER (TYPE 1) (BY SIMILARITY).  
 FT CARBOHYD 66 66 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 109 109 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 186 186 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 231 231 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 280 280 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 395 395 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT VARIANT 42 42 P -> S.  
 FT VARIANT 119 119 H -> R.  
 FT VARIANT 246 246 R -> S.  
 FT VARIANT 256 256 P -> L.  
 FT VARIANT 261 261 P -> A.  
 SO SEQUENCE 531 AA; 57545 MW; 737339803F75AB19 CRC64;

Query Match 17.9%; Score 564; DB 1; Length 531;  
 Best Local Similarity 30.8%; Pred. No. 7.9e-33;  
 Matches 174; Conservative 62; Mismatches 171; Indels 158; Gaps 27;

QY 25 VDSPTGVNRYPTLTLEVDNMTGPDGVNKEKVLVNNSTIGPTIFADMGDTIQVYINN 84  
 DB 14 VSTRPFAVNRKTFEDINVN--VAPDG-FORPIVSVNGLVPGTLLITANKGDTLRINVTNQ 70  
 QY 85 LE---TNGTSIHWHGKHOKGTNLHDGANGITECPRPKGGKRYRKAQ---OYGTSMY 137  
 DB 71 LTDPSPMRATTIHHGGLFQATLADDEGPATYQCP---AQNLSYIEIPLHGOTIMNY 127  
 QY 138 HSHPSAOGVGVGAID---NGPASILPYDT--LGVPIISDYYSADLVE--LTKN 189  
 DB 128 HAHLASQYVGLNRPVLYIDPNPHKRSRYDDVASTVVMLEDMYHTPAVLEKQMFSTNN 187  
 QY 190 SG--APESDNLVNGSTAKHPETGEGEVANTLP-----GRRHRLRLINTSVENHFQ 239  
 DB 188 TALISPPVDSGLN-----GGRYVGGPVRVRSYINVRGRKRYRLRVINASAGISFT 239  
 QY 240 VSLVNHMTCTIADMVVNATVDSLFLGVGORYVYIEANRTPGNMFN--VTFGGGLL 297  
 DB 240 FSTIEGRLTYIENDGIRPHOLPVDSPQIYAGORSYIVTEANQTANWIRAPMTVAG--- 296  
 QY 298 CGGSRNTPA---AIFHYAGPGCPPTDE-----GKAPVDHNCIDLPLKRVVARDVPLS 349  
 DB 297 AGTNANLDPNIVFAVLHTEGAPNAEPTEEGSAIGTALVEENLHALIN----- 344  
 QY 350 GFAKRAUNDTLDVTLTGTPLFVWKGSA-----INIDGRAVVDVYL-----ON 396  
 DB 345 -----PGAP-----GGSAPADVSLNLAIGRSTYVDSILKFTFNNTIYEA 382  
 QY 397 TSPPPGTIVVEVNGADQWSTWLIENDPAPPT-----LP-----HPMHL 435  
 DB 383 PSLEPTLLKILANNAS-----ND--ADFTPNEHTIVLPNNKVIGAQHHRGADIPHL 431  
 QY 436 HGHDFYV---LGRSPDPSASNEHNVDPARDAQLLSGANVVRDVSMLPAFGWVLSFR 492

DB 432 HGHDFIVKSLGCTPNY-----VMPRRDVRVVGCTG-VVLRFK 469  
 QY 493 ADNPGANLFRCHT--AMHVSGLGV 515  
 DB 470 ADNPGPWFVCHCHDCTWRIGSLSL 494

Search completed: December 4, 2002, 10:45:37  
 Job time: 16 secs

DE	16-OCT-2001 (Rel. 40, Last annotation update)
DT	Laccase 2 precursor (EC 1.10.3.2) (benzenediol:oxygen oxidoreductase)
DE	(ligninol oxidase) (diphenol oxidase) (laccase I).
GN	LCC2 OR LCCI.
OS	Trametes versicolor (White-rot fungus).
OC	Eukaryota; Fungi; Basidiomycota; Hymenomycetes; Homobasidiomycetes;
OC	Applikophorales; Trametes.
OX	NCBI_TaxID=5325;
RN	[1]
RP	SEQUENCE FROM N.A.
RC	STRAIN=52j;
RX	MEDLINE=97464057; PubMed=9322748;
RA	Ong E., Pollock W.B., Smith M.;
RT	"Cloning and sequence analysis of two laccase complementary DNAs from
RL	the ligninolytic basidiomycete Trametes versicolor.";
CC	Gene 196:113-119(1997).
CC	-1- FUNCTION: LIGNIN DEGRADATION AND DETOXIFICATION OF LIGNIN-DERIVED
CC	PRODUCTS (PROBABLE).
CC	-1- CATALYTIC ACTIVITY: 4 benzenediol + O(2) = 4 benzosquinone + 2
CC	H(2)O.
CC	-1- COFACTOR: BINDS 4 CU-IONS PER MOLECULE. THREE DISTINCT CU
CC	CENTERS KNOWN AS TYPE 1 OR BLUE, TYPE 2 OR NORMAL, AND TYPE
CC	3 OR COUPLED BINUCLEAR (BY SIMILARITY).
CC	-1- SUBCELLULAR LOCATION: Secreted.
CC	-1- SIMILARITY: BELONGS TO THE FAMILY OF MULTICOOPER OXIDASES.
CC	-1- SIMILARITY: CONTAINS 3 PLASTOCYANIN-LIKE DOMAINS.
CC	-----
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration
CC	between the Swiss Institute of Bioinformatics and the EMBL Outstation -
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CC	or send an email to <a href="mailto:license@isb-sib.ch">license@isb-sib.ch</a> .
CC	-----
DR	EMBL; U44851; AAA86659.1; .
DR	EMBL; U44430; AAC49828.1; .
DR	HSSP; P37064; IAOZ.
DR	InterPro; IPRO02355; Cu-oxidase.
DR	InterPro; IPRO02355; Multicu_oxidse2.
DR	Pfam; PF00394; Cu-oxidase; 3.
DR	PROSITE; PS00079; MULTICOOPER_OXIDASE1; 1.
DR	PROSITE; PS00080; MULTICOOPER_OXIDASE2; FALSE NEG.
KW	Oxidoreductases; Signal; Copper; Metal-binding; Glycoprotein; Repeat;
KW	Lignin degradation; Multigene family;
FT	SIGNAL 1 20 POTENTIAL.
FT	CHAIN 21 519 LACCASE 2.
FT	DOMAIN 22 147 PLASTOCYANIN-LIKE 1.
FT	DOMAIN 159 301 PLASTOCYANIN-LIKE 2.
FT	DOMAIN 368 490 PLASTOCYANIN-LIKE 3.
FT	METAL 84 84 COPPER (TYPE 2) (BY SIMILARITY).
FT	METAL 86 86 COPPER (TYPE 3) (BY SIMILARITY).
FT	METAL 129 129 COPPER (TYPE 3) (BY SIMILARITY).
FT	METAL 131 131 COPPER (TYPE 3) (BY SIMILARITY).
FT	METAL 415 415 COPPER (TYPE 1) (BY SIMILARITY).
FT	METAL 418 418 COPPER (TYPE 2) (BY SIMILARITY).
FT	METAL 420 420 COPPER (TYPE 3) (BY SIMILARITY).
FT	METAL 422 422 COPPER (TYPE 3) (BY SIMILARITY).
FT	METAL 473 473 COPPER (TYPE 1) (BY SIMILARITY).
FT	METAL 474 474 COPPER (TYPE 3) (BY SIMILARITY).
FT	METAL 478 478 COPPER (TYPE 1) (BY SIMILARITY).
FT	METAL ? ? COPPER (TYPE 1) (BY SIMILARITY).
FT	METAL ? ? COPPER (TYPE 1) (BY SIMILARITY).
FT	CARBOHYD 74 74 N-LINKED (GLCNAC . . ) (POTENTIAL).
FT	CARBOHYD 161 161 N-LINKED (GLCNAC . . ) (POTENTIAL).
FT	CARBOHYD 228 228 N-LINKED (GLCNAC . . ) (POTENTIAL).
FT	CARBOHYD 237 237 N-LINKED (GLCNAC . . ) (POTENTIAL).
FT	CARBOHYD 271 271 N-LINKED (GLCNAC . . ) (POTENTIAL).
FT	CARBOHYD 353 353 N-LINKED (GLCNAC . . ) (POTENTIAL).
FT	CARBOHYD 361 361 N-LINKED (GLCNAC . . ) (POTENTIAL).
FT	CARBOHYD 456 456 N-LINKED (GLCNAC . . ) (POTENTIAL).
FT	CARBOHYD 459 459 D->V (IN REF.1; AAC49828).
SO	SEQUENCE 519 AA; 53810 MW; BFB5B4CD0007702 CRC64;

Query Match 18.0% Score 570; DB 1; Length 519;  
Best Local Similarity 29.9%; Pred. No. 2.9e-33;  
Matches 163; Conservative 73; Mismatches 201; Indels 108; Gaps 22;

OY	49	PDCVVKKVMVLVNNSIIIPTEFADMGDTIIV-----TVINNNLETNGSTIHMHGLHOKGTNL	104
Dd	37	PDGFLRLADI-VNNGVVPSPLTIKKKGDRPOLNVDDTLTNHSMLKTSISGHMHPFPAGTGW	95
OY	105	HDSANGITECPPIPKGKRKYEFKA-QQYGSYWSHSPSAOYGCVGAIOI---NGPAS	160
Dd	96	ADGPFAFNOCPT-ASGSHFYLDFFHYPPDOAGFEWYSHSISTOCDELKPFFVYDDEKDPHA	154
OY	161	LPEYDD--LGEFPIIDYYSSADELYELTKNSGARF---SDNWLEFGNAKHETGEGEXA	215
Dd	155	SKRYDVNESITYITLLDMWHITA-----RLGRPFPGADRTITINGCRSASTFTALAA	206
OY	216	NVTLPFRRRHLRLINTSVENHFOYSILVNHWCIIAADMVPNAMATVDLSLEGVGORYDY	275
Dd	207	VINVQHGRKRYRPRILVISICDPNYTFPSIDGNHLTVIEVDGINSQLPDLVDSIQIFAQRYSF	266
OY	276	VIEARTGTGNWF--NTTFGGSLLOGSGRNRPRAIFRYAGAPEGPPIDEKGAPVDHACL	333
Dd	267	VLNAQPTGVGNWVRANPNFYGVFAGJLN---SAILRKOGAPVAEPPTTOTSY-----	317
OY	334	DLP-----NLKPVVADVPLSCGFARADWTLDLTDTCTPLRVMMVNGSA-----I	380
Dd	318	-IPLETMLNPRLARNRPHVPGPSPTPGCVDRKANLAEAFENGSTNF---INNATTPTTPVPLL	373
OY	381	NIDMRNAVVDVYLTONTSFP-PGYIIVEVNCADOWSTYLIENDPCARPRTLPHPMHLHGHD	439
Dd	374	QLLSAQTAODDLLPAGSYVPLPANSTIEI-----TLPATALLAPA---PAHFHLGHA	423
OY	440	FYVLGRSPDESASPASNERHVDFPARDAG--LLSGANPVRDY--SWLRPAFG-WVVSFRAD	494
Dd	424	FAYV-----RAGSTTYNDPIRDVYSTGTPAAGDWTTIRFORTD	464
OY	495	NEGAVLFHCIIAHMVSGLVGYLERADDLCQAVIDADADDIDLCDMRRXYMPNYPYK	554
Dd	465	NPGEFLFHCHIDFIHDAFGAIIVADFADVADYAA-----NPPVK	502
OY	555	SDSGL	559
Dd	503	AMS DL	507

RESULT 14  
LACS\_THACU STANDARD; PRT: 572 AA.

ID	LACS_THACU	STANDARD:	PRT: 572 AA.
AC	002079;		
DT	01-NOV-1997 (Rel. 35, Created)		
DT	01-NOV-1997 (Rel. 35, Last annotation update)		
DT	01-NOV-1997 (Rel. 35, Last annotation update)		
DE	Laccase 3 precursor (EC 1.10.3.2) (Benzenediol:oxygen oxidoreductase)		
DN	(Urishiol oxidase) (Diphenol oxidase).		
GN	LCC3.		
OS	Thanatephorus cucumeris (Black scurf of potato) (Rhizoctonia solani).		
OC	Eukaryota; Fungi; Basidiomycota; Hymenomyces; Heterobasidiomycetes;		
OC	Heterobasidiomycetidae; Ceratobasidiales; Ceratobasidiaceae;		
OC	Mitosporic Ceratobasidiaceae; Rhizoctonia.		
RX	NCBI_TaxID=107832;		
RM	[1]		
RP	SEQUENCE FROM N.A.		
RC	STRAIN-RS22;		
KX	MEDLINE=96171523; PubMed=8598061;		
RA	Walkeither J.A., Xu F., Brown K.M., Brown S.H., Golightly E.J.,		
RT	Halter T., Kauppinen S., Pederson A., Schneider P.;		
RT	"The identification and characterization of four laccases from the		
RL	plant pathogenic fungus Rhizoctonia solani.";		
Curr. Genet.	29:395-403(1996).		
-I-	FUNCTION: LIGNIN DEGRADATION AND DETOXIFICATION OF LIGNIN-DERIVED		
PRODUCTS (PROBABLY).			
-I-	CATALYTIC ACTIVITY: 4 benzenediol + O(2) = 4 benzosemiquinone + 2		
CC	H(2)O.		

QY 145 YGNGVCAIOLNIP-----ASTL-PYDIDLGVFPISDYYSSADELVELTKNSGAPF-----SD 196  
 Db 139 YCDGLRPLVYPPDDANSLYVDVDDTYITLADWHTHA-----KLGRAPFRGPD 190  
 QY 197 NVLENGTAKHPETGEG--EYANVTLPGRRRRLRLNTSVENHFOVSLVHNTMCIIAAM 254  
 Db 191 SVLNGIGRSGDGGATNLTIVTGKRRYRFLVLSICDPNFTSIDGHNMHTIEVGD 250  
 QY 255 VPPNANMVDLSLFGVGRVYVIEANTPGNYFNV-----TFEGGILCGSSRRPY 306  
 Db 251 VNHEDALDVDSIQIFAGGRSFTILNANOSIDNYMTRALPNTGTTDTTGG-----VN 300  
 QY 307 AALFHYAGAGGPPTEDEKAPV-----DHNCIDLPLNKPVAVRDPVLSGFAKRAADNTLDVT 362  
 Db 301 SALIRYDTAEIDETNTATTSVPLPFTDLVPLDN--PAAPGDPQVGG-----VDLAMSID 354  
 QY 363 LDFTTGPLEV-----MKVNGSAINIDMGRAVVDVYLQNT 397  
 Db 355 FSENGSNFETINNETEVEPVVLLQILSGADAASILPNSGV-----YTLPSNS 403  
 QY 398 SFPFGYIVENVGADOMSTYLIENDPGAPTLRPHMLHGHDFYVLSRSPDESPASNERH 457  
 Db 404 TIEISFPIITTDG-----VLNAPGA-----PHEFLHGHITSV-----437  
 QY 458 VDPDARDAG--LLSGANPVRD--VSMPLPAGVWVLSFRADNPGAMLPHCHIAHVSGLG 514  
 Db 438 -----RSGSSTFNYPANPVRDVTSGNSGDNTVIRTTNPNCGWFLHCHIDHLENGFA 492  
 QY 515 VVYLERADLRGAVSDADDDRLCADMRWPTNPYKSDS 557  
 Db 493 IVNGE-----DPAATFASANPVPAMSDLPCT--YDALDS 524

RESULT 11  
 LACS\_TRAVE STANDARD; PRT; 527 AA.  
 ID LACS\_TRAVE  
 AC 012717;  
 DT 01-NOV-1997 (Rel. 35, Created)  
 DT 01-NOV-1997 (Rel. 35, Last sequence update)  
 DT 15-JUL-1999 (Rel. 38, Last annotation update)  
 DE Laccase 5 precursor (EC 1.10.3.2) (Benzenediol: oxygen oxidoreductase)  
 GN (urishiol oxidase) (Diphenol oxidase) (Laccase IV).  
 OS LCC5 OR LCCIV.  
 OS Trametes versicolor (White-rot fungus).  
 OC Eukaryota; Fungi; Basidiomycota; Hymenomycetes; Homobasidiomycetes;  
 OC Aphyllophorales; Trametes.  
 ON NCBI\_TaxID=5325;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=52J;  
 RX MEDLINE=97464057; PubMed=9322748;  
 RA Ong E., Pollock W.B., Smith M.;  
 RT "Cloning and sequence analysis of two laccase complementary DNAs from  
 the ligninolytic basidiomycete trametes versicolor \*";  
 RL Gene 196:113-119(1997).  
 CC -1- FUNCTION: LIGNIN DEGRADATION AND DETOXIFICATION OF LIGNIN-DERIVED  
 CC PRODUCTS (PROBABLE).  
 CC -1- CATALYTIC ACTIVITY: 4 benzenediol + O(2) -> 4 benzosemiquinone + 2  
 CC H(2)O.  
 CC -1- COFACTOR: BINDS 4 CU-IONS PER MOLECULE. THREE DISTINCT CU  
 CC CENTERS KNOWN AS TYPE 1 OR BLUE, TYPE 2 OR NORMAL, AND TYPE  
 CC 3 OR COUPLED BINUCLEAR (BY SIMILARITY).  
 CC -1- SUBCELLULAR LOCATION: Secreted.  
 CC -1- SIMILARITY: BELONGS TO THE FAMILY OF MULTICOPPER OXIDASES.  
 CC -1- SIMILARITY: CONTAINS 3 PLASTOCYANIN-LIKE DOMAINS.

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 CC EMBL, U44431; AAC9829.1; -.  
 DR HSSP; P37064; IAOZ.  
 DR InterPro; IPR001117; Cu-oxidase.  
 DR InterPro; IPR002355; MultiCu\_oxidase2.  
 DR Pfam; PF00394; Cu-oxidase; 3.  
 DR PROSITE; PS00079; MULTICOPPER\_OXIDASE1; 1.  
 DR PROSITE; PS00080; MULTICOPPER\_OXIDASE2; FALSE\_NEG.  
 KW Oxidoreductase; Signal; Copper; Metal-binding; Glycoprotein; Repeat;  
 KW Lignin degradation; Multigene family.  
 FT SIGNAL 1  
 FT CHAIN 24  
 FT DOMAIN 25  
 FT DOMAIN 150  
 FT DOMAIN 162  
 FT DOMAIN 306  
 FT DOMAIN 373  
 FT METAL 87  
 FT METAL 89  
 FT METAL 132  
 FT METAL 133  
 FT METAL 134  
 FT METAL 142  
 FT METAL 425  
 FT METAL 428  
 FT METAL 430  
 FT METAL 430  
 FT METAL 480  
 FT METAL 481  
 FT METAL 482  
 FT METAL 486  
 FT METAL 486  
 FT CARBOHYD 74  
 FT CARBOHYD 77  
 FT CARBOHYD 156  
 FT CARBOHYD 209  
 FT CARBOHYD 233  
 FT CARBOHYD 242  
 FT CARBOHYD 276  
 FT CARBOHYD 317  
 FT CARBOHYD 358  
 FT CARBOHYD 366  
 FT CARBOHYD 393  
 FT CARBOHYD 402  
 FT CARBOHYD 464  
 FT CARBOHYD 464  
 SQ SEQUENCE 527 AA; 56094 MW; D9597491F1F79825 CRC64;

Query Match 18.4%; Score 580.5; DB 1; Length 527;  
 Best local Similarity 30.5%; Pred. No. 5.3e-34;  
 Matches 178; Conservative 65; Mismatches 203; Indels 137; Gaps 26;

QY 31 GVVYRPYT-LTLEVDNMTGPDGVYKREKVMLVNNSITGPTTFADWGDRTIQVTVINLT--ET 87  
 Db 23 GAIGPVYTLDTISNAD--VPEPDGITRAV--LAGGVFPEPLITGNKGDFQVNTVDNLNET 79  
 QY 88 --NCTSIHMHGLOKGNLHDGANGITECP1PPKGGKRYRFA--QOYGSWHSHP 144  
 Db 80 MKSTTIHMHGIPQAGTNMADGAFFVQCPI--ATGNSFLDFTVPDAGCFVHSHLSIQ 138  
 QY 145 YGNGVCAIOLNIP-----ASTL-PYDIDLGVFPISDYYSSADELVELTKNSGAPF-----SD 196  
 Db 139 YCDGLRPLVYPPDDANSLYVDVDDTYITLADWHTHA-----KLGRAPFRGPD 190  
 QY 197 NVLENGTAKHPETGEG--EYANVTLPGRRRRLRLNTSVENHFOVSLVHNTMCIIAAM 254  
 Db 191 SVLNGIGRSGDGGATNLTIVTGKRRYRFLVLSICDPNFTSIDGHNMHTIEVGD 250  
 QY 255 VPPNANMVDLSLFGVGRVYVIEANTPGNYFNV-----TFEGGILCGSSRRPY 306  
 Db 251 VNHEDALDVDSIQIFAGGRSFTILNANOSIDNYMTRALPNTGTTDTTGG-----VN 300  
 QY 307 AALFHYAGAGGPPTEDEKAPV-----DHNCIDLPLNKPVAVRDPVLSGFAKRAADNTLDVT 362  
 Db 301 SALIRYDTAEIDETNTATTSVPLPFTDLVPLDN--PAAPGDPQVGG-----VDLAMSID 354  
 QY 363 LDFTTGPLEV-----MKVNGSAINIDMGRAVVDVYLQNT 397

QY	30	TGVVAPRY-LITLLEDMNTGPGGVKKEVYMLVNNISICTPTLEADMGGDIOQVYVNLN--E	86
Db	21	SAAGPVPYDILFISNGD--VSPDGFRAAV-LANGVFEPRLTGKMGQNFQINVIDNLISNE	77
QY	87	T--NCTSIHMGICLHCKGNTLNDGANGITIECPRIPEKGGKRYRFA--QOQTSVYHSFSA	14
Db	78	TMKSTSIHMGIEFGKGNMADGAAPVOCPT-ATGNSFLYDFATDQAGFWHSHLST	136
QY	144	QYGNVGVAIQINGPASTLPY-----DNDLGVPISDYVSSADELYELFTRNSGAF--	194
Db	137	QYCDGLRBPVNVYDPSD--PHADLYVDDEETITITLSDWYHTAA-----SLGAAPF IG	18
QY	135	SDNVLENGTAKHREGEDEBEAYVTLTPGRHRLRLINTSVENHPQVLSVNHPTKICLADM	255
Db	188	SDSTLITNGIRPAGGSDTDLAYITVEQGRKRYRMRLTSLCDPNVFSIDGHNMTITEADA	247
QY	255	VPVNMTADSLFLAGORARDVYIEANRPYGNWYF-----NVTGEGGILCGGSRNRPRA	307
Db	248	VNHEPRLTQSDIQIYAGORSFVLGTADODIDNFEIPLRPSAGTSPDGCI-----NS	296
QY	308	ALFNHAGPGRPRDEGKAPYDHNCLDLPLNKRVYAROVYLSGFAKRAKDNTLDYLTDTG	367
Db	299	ALIKRSQGSSEVDPTTETTSV--LPLEDRANLPRLSPAPGDPNIGVDYALMIDFENDG	356
QY	368	TPLEWYKVNGSALINDWGRAVVDYVLTGNTS---FPPG-YNIVEVNGADQMWYL-IEN	422
Db	357	TNFFINDVSFVSPVY----PYLLDILSTTSADLLPFGSLFAVPSNSTIETISPTPATN	411
QY	422	DPGAFPTLPHPHNLGHDPYVUGSRPDSPASNEKHVDPDRAIDGL--LSGANPRRQVS	475
Db	413	APGA-----PHPHNLGHFTSY-----RTAGSTPTNRYNVPYRQDV	444
QY	480	MLPARG-VWVLSFRADPGAMLFCHILAMHVSGGLGVYLERADLRKAGVSDADADDLDR	538
Db	450	MTGIVGDVNTYINFTDNDGMPWFLHCHIDHLEAGFAIVESEDTADVSNTPPTPSTA----	504
QY	539	LCADMRRTYPT-NPYKPSD	556
Db	505	----WEDLCPTYNALDSSD	519

ID	LOC2_TRAVE	STANDARD:	PRF:	520 AA.
AC	012719;			
AD	01-NOV-1997 (Rel. 35, Created)			
DT	01-NOV-1997 (Rel. 35, Last sequence update)			
DT	01-NOV-1997 (Rel. 35, Last annotation update)			
DE	Laccase 4 precursor (EC 1.10.3.2) (benzenediol:oxygen oxidoreductase)			
DE	(Urishiol oxidase) (Diphenol oxidase).			
CN	LC64 OR LC61			
OS	Trametes versicolor (White-rot fungus).			
OC	Eukaryota; Fungi; Basidiomycota; Hymenomycetes; Homobasidiomycetes;			
OC	Asphyllophorales; Trametes.			
OX	NCBI_TaxID=53325;			
RM	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=PRL 572;			
RX	MEDLINE=95399443; PubMed=766913;			
RA	Joensson L.J., Sjoestrom K., Haegstroem I., Nyman P.O.;			
RT	"Characterization of a laccase gene from the white-rot fungus			
RT	Trametes versicolor and structural features of basidiomycete			
RT	laccases.";			
RL	Biochim. Biophys. Acta 1251:210-215(1995).			
CC	-1- FUNCTION: LIGNIN DEGRADATION AND DETOXIFICATION OF LIGNIN-DERIVED			
CC	PRODUCTS (PROBABE).			
CC	-1- CATALYTIC ACTIVITY: 4 benzenediol + O(2) = 4 benzosemiquinone + 2			
CC	H(2)O.			
CC	-1- COFACTOR: BINDS 4 CU-IONS PER MOLECULE. THREE DISTINCT CU			
CC	CENTERS KNOWN AS TYPE 1 OR BLUE, TYPE 2 OR NORMAL, AND TYPE			
CC	3 OR COUPLED BINUCLEAR (BY SIMILARITY).			
CC	-1- SUBCELLULAR LOCATION: Secreted.			
CC	-1- SIMILARITY: BELONGS TO THE FAMILY OF MULTICOPPER OXIDASES.			
CC	-1- SIMILARITY: CONTAINS 3 PLASTOCYANIN-LIKE DOMAINS.			
CC	-----			
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CC	between the Swiss Institute of Bioinformatics and the EMBL outstation -			
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CC	or send an email to <a href="mailto:license@sib-sib.ch">license@sib-sib.ch</a> ).			
CC	-----			
DR	EMBL; X84683; CAA59161.1; -			
DR	HSSP; P37064; IAOZ.			
DR	InterPro; IPR001117; Cu-oxidase.			
DR	InterPro; IPR002355; Multicu_oxidase2.			
DR	Pfam; PF00394; Cu-oxidase; 3.			
DR	PROSITE; PS00079; MULTICOPPER_OXIDASE1; 1.			
DR	PROSITE; PS00080; MULTICOPPER_OXIDASE2; FALSE NEG.			
KW	oxidoreductase; Signal; Copper; Metal-binding; Glycoprotein; Repeat;			
KW	Lignin degradation; Multigene family			
FT	SIGNAL	1..22	POTENTIAL.	
FT	CHAIN	23..520	LACCASE 4.	
FT	DOMAIN	24..149	PLASTOCYANIN-LIKE 1.	
FT	DOMAIN	161..303	PLASTOCYANIN-LIKE 2.	
FT	DOMAIN	370..491	PLASTOCYANIN-LIKE 3.	
FT	DISULFID	107..509	PROBABE.	
FT	DISULFID	139..227	PROBABE.	
FT	METAL	86..86	COPPER (TYPE 2) (BY SIMILARITY).	
FT	METAL	88..88	COPPER (TYPE 3) (BY SIMILARITY).	
FT	METAL	131..131	COPPER (TYPE 3) (BY SIMILARITY).	
FT	METAL	133..133	COPPER (TYPE 3) (BY SIMILARITY).	
FT	METAL	418..418	COPPER (TYPE 1) (BY SIMILARITY).	
FT	METAL	421..421	COPPER (TYPE 2) (BY SIMILARITY).	
FT	METAL	423..423	COPPER (TYPE 3) (BY SIMILARITY).	
FT	METAL	473..473	COPPER (TYPE 3) (BY SIMILARITY).	
FT	METAL	474..474	COPPER (TYPE 1) (BY SIMILARITY).	
FT	METAL	475..475	COPPER (TYPE 3) (BY SIMILARITY).	
FT	METAL	479..479	COPPER (TYPE 1) (BY SIMILARITY).	
FT	METAL	?	COPPER (TYPE 1) (BY SIMILARITY).	
FT	CARBOHYD	73..73	N-LINKED (GLCNAC. . .) (POTENTIAL).	
FT	CARBOHYD	76..76	N-LINKED (GLCNAC. . .) (POTENTIAL).	
FT	CARBOHYD	239..239	N-LINKED (GLCNAC. . .) (POTENTIAL).	
FT	CARBOHYD	399..399	N-LINKED (GLCNAC. . .) (POTENTIAL).	
FT	CARBOHYD	457..457	N-LINKED (GLCNAC. . .) (POTENTIAL).	

```
CC Aphylllophorales; Trimateles.
OX NCBI_TaxID=47662; [1]
RN SEQUENCE FROM N.A.
RC TISSUE=Mycellium;
RX MEDLINE=97076915; PubMed=8975613;
RA Yaver D.S., Xu F., Golightly E.J., Brown K.M., Brown S.H.,
RT Ray M.W., Schneider P., Halkier T., Mondorf K., Dalboe H.;
    "Purification, characterization, molecular cloning, and expression of
two laccase genes from the white rot basidiomycete trimateles
villosoa.";
FT Appl. Environ. Microbiol. 62:834-841(1996).
CC -I- FUNCTION: LIGNIN DEGRADATION AND DETOXIFICATION OF LIGNIN-DERIVED
PRODUCTS (PROBABLE).
CC CC
CC -I- CATALYTIC ACTIVITY: 4 benzenediol + O(2) = 4 benzosemiquinone + 2
H2/O.
CC -I- COFACTOR: BINDS 4 CU-IONS PER MOLECULE. THREE DISTINCT CU
CENTERS KNOWN AS TYPE 1 OR BLUE, TYPE 2 OR NORMAL, AND TYPE
3 OR COUPLED BINUCLEAR (BY SIMILARITY).
CC -I- SUBUNIT: HOMODIMER.
CC -I- SUBCELLULAR LOCATION: Secreted.
CC -I- SIMILARITY: BELONGS TO THE FAMILY OF MULTICOOPER OXIDASES.
CC -I- SIMILARITY: CONTAINS 3 PLASTOCYANIN-LIKE DOMAINS.
-----
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or send an email to license@isb-sib.ch).
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CC EMBL; LA9376; AAC41686.1; -.
DR HSSP; P37064; 1A0Z.
DR InterPro; IPR001117; Cu-oxidase.
DR InterPro; IPR002355; MulticCu_oxidse2.
DR Pfam; PF00394; Cu-oxidase; 3.
DR PROSITE; PS00079; MULTICOOPER_OXIDAS1; 1.
DR PROSITE; PS00080; MULTICOOPER_OXIDAS2; FALSE_NEG.
KW Oxidoreductases; Signal; Copper; Metal-binding; Glycoprotein; Repeat;
KW Lignin degradation; Multigene family.
KV SIGNAL 1 21 POTENTIAL.
FT CHAIN 1 22 520 LACCASE 1.
FT DOMAIN 23 148 PLASTOCYANIN-LIKE 1.
FT FT DOMAIN 160 302 PLASTOCYANIN-LIKE 2.
FT METAL 369 491 PLASTOCYANIN-LIKE 3.
FT METAL 85 85 COPPER (TYPE 2) (BY SIMILARITY).
FT METAL 87 87 COPPER (TYPE 3) (BY SIMILARITY).
FT METAL 130 130 COPPER (TYPE 3) (BY SIMILARITY).
FT METAL 132 132 COPPER (TYPE 3) (BY SIMILARITY).
FT METAL 416 416 COPPER (TYPE 1) (BY SIMILARITY).
FT METAL 419 419 COPPER (TYPE 2) (BY SIMILARITY).
FT METAL 421 421 COPPER (TYPE 3) (BY SIMILARITY).
FT METAL 423 423 COPPER (TYPE 3) (BY SIMILARITY).
FT METAL 473 473 COPPER (TYPE 3) (BY SIMILARITY).
FT METAL 474 474 COPPER (TYPE 1) (BY SIMILARITY).
FT METAL 475 475 COPPER (TYPE 3) (BY SIMILARITY).
FT METAL 479 479 COPPER (TYPE 1) (BY SIMILARITY).
FT METAL ? ? COPPER (TYPE 1) (BY SIMILARITY).
FT CARBOHYD 72 72 N-LINKED (GLCNAC . . ) (POTENTIAL).
FT CARBOHYD 75 75 N-LINKED (GLCNAC . . ) (POTENTIAL).
FT CARBOHYD 229 229 N-LINKED (GLCNAC . . ) (POTENTIAL).
FT CARBOHYD 238 238 N-LINKED (GLCNAC . . ) (POTENTIAL).
FT CARBOHYD 354 354 N-LINKED (GLCNAC . . ) (POTENTIAL).
FT CARBOHYD 361 361 N-LINKED (GLCNAC . . ) (POTENTIAL).
FT CARBOHYD 457 457 N-LINKED (GLCNAC . . ) (POTENTIAL).
SQ SEQUENCE 520 AA; 55545 MW; 046ABBD74737C60E CRC64;.
Query Match 20.1%; Score 636; DB 1; Length 520;
Best Local Similarity 33.0%; Pred.No.=5;Se=38;
Matches 184; Conservative 69; Mismatches 204; Indels 100; Gaps 24.
QY 31 GVVRPTTLLEVDNMTGDSGVVKEKVALVNNSITIGPTPADWGDTIOVTYNNLETN-- 88
| | : | | | | : | | | : | | : | | : | | : | | : |
```

Db	24	GPVADLTITNAAY-----SPDEFSRQAV-VVNGGTPPGRLITNSMGDRQLVNIIDLNIHTM	78
Oy	89	--GTSIHNHGHLQKGTNLHDANGITEEPRIIPKSGKRYRKA-QOYGTSMYSHSFSAOY	145
Db	79	VKSTSIHHNGFFQKGTNNADPAPFIMCCPI--SSHSPLFLQYQVDPDQAGTMYHSHLSTQY	137
Oy	146	GNGVGATQI---NGPASI.PYDTDLG--VPFISDYVSSADELVELTKNSGAPF---SDN	197
Db	138	CDGLGRFPVVYDPRADPRADLYDVNDQVYIILVDMYHAA-----KLGAPPLGADA	169
Oy	198	VLFNGTANHPETGECEANVTLLPGRRRLRLINTSYENHFQVSLVNHITMCITIAADV	257
Db	190	TLINCKGRSPSTTTADLSVITVTEPGKRFRFLYSICSDPNFTFSDGHNMTHIIETDSINT	249
Oy	258	NAMVYDSLFLVGQRXYDVIANTEPQWYF--WVTGCGILCGSGSNPPAALFHNAGA	315
Db	250	APLVYDS.IQIIPAAQYSFVLEANAQVDMYIARAPNENGNGETGIN---SAILRIDGA	305
Oy	316	PGGPPT---DEGKAPVDNHCIDLNLKRVYVARDPLSGFAKRAANTLDVLTDTGTFLEV	372
Db	306	AAVEPTTQTSTTAP-----LNEVNLHPLVTVAVPGSVAGGVDLAINMAFNENGTFE-	355
Oy	373	WKVNGSAINIDMGRAVDYVL-TQNTS--FPPG--YNIIVEYNGADQMSYMLIENDPGAPF	422
Db	360	--INQSTPEPTPVYLIQIISGAONAODLLPFGSVYSLPS--NADIEISFPTAAAPG--	414
Oy	428	TLPHMHHLGHDEFYILGSPDESPASNERHVFEDPARDG--LISGAPVVRDY--SM.LPA	483
Db	415	--PHEFHILGHAFANV-----RSGSVYVYNDPIFPDYVSTGTPA	455
Oy	484	FG-VWVLSFRADNPGAWLPHCHIANHWSGICGVYLLERADLRCAVSDADADDLRLCAD	543
Db	454	AGDNTVITFRFDNDEPWFHLGHIFLEKRAVYVAEDIPDVASA-----	498
Oy	543	WRRYPTNRYPKRSDGL 559	
Db	499	-----NPVQAMSDL 508	
RESULT 7			
LACL CORHI			
ID	LACL CORHI	STANDARD;	PRT; 520 AA.
AC	002497;		
DT	01-OCT-1996 (Rel. 34, Created)		
DT	01-OCT-1996 (Rel. 34, Last sequence update)		
DT	01-OCT-2001 (Rel. 40, Last annotation update)		
DE	Laccase precursor (EC 1.10.3.2) (Benzenediol: oxygen oxidoreductase)		
DE	(Urisinol oxidase) (Ligninolytic phenoloxidase).		
OS	Coriolus hirsutus.		
OC	Eukaryota; Fungi; Basidiomycota; Hymenomycetes; Homobasidiomycetes;		
OC	Applihophorales; Coriolus.		
OX	NCBI_TaxID=5327;		
RN	(1)		
RP	SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.		
RC	STRAIN-IFO 4917;		
RX	MEDLINE=90368706; PubMed=2394718;		
RA	Kojima Y., Tsukuda Y., Kawai Y., Tsukamoto A., Sugiura J.,		
RA	Sakano M., Kita Y.;		
RT	"Cloning, sequence analysis, and expression of ligninolytic		
RT	phenoloxidase genes of the white-rot basidiomycete Coriolus		
RT	hirsutus.";		
RL	J. Biol. Chem. 265:15224-15230(1990).		
CC	-1- FUNCTION: MOST PROBABLY PLAYS AN IMPORTANT ROLE IN LIGNIN		
CC	DEGRADATION. CLEAVES THE C-C AND C-O BONDS OF SOME PHENOLIC LIGNIN		
CC	MODEL COMPOUNDS (SUCH AS O- AND P-QUINOLS, AMINOPHENOLS AND		
CC	PHENYLENEDIAMINE).		
CC	-1- CATALYTIC ACTIVITY: 4 benzenediol + O(2) = 4 benzosemiquinone + 2		
CC	H(2)O.		
CC	-1- COFACTOR: BINDS 4 CU-IONS PER MOLECULE. THREE DISTINCT CU		
CC	CENTERS KNOWN AS TYPE 1 OR BLUE, TYPE 2 OR NORMAL, AND TYPE		
CC	3 OR COUPLED BINUCLEAR.		
CC	-1- SUBCELLULAR LOCATION: Secreted.		
CC	-1- POLYMORPHISM: 2 ALLELIC FORMS VARYING IN ONE AA POSITION.		



Best Local Similarity 63.8%; Pred. No. 2e-136;  
Matches 356; Conservative 83; Mismatches 113; Indels 6; Gaps 2;

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OY 4 CNTPSRACCTDGVDTVDVENDSPDGVVPTLTITLTDVNTGPGVYKEMVLYNNS 63
   ||:|||||:|:|||||:|:|||||:|:|||||:|:|||||:|:|||||:|:|||||:|:
Db 55 CNSPTNQCSPSPFNINTDELGTPTNGKTRRYKLTLETEDNMIGPGGVKIDKVMVNDN 114
   ||:|||||:|:|||||:|:|||||:|:|||||:|:|||||:|:|||||:|:|||||:|:
OY 64 IIPPTJFADGDTIOVYVNNLETNGTSHHGHGKGTMLHDGANGITECPIPPKGRK 123
   ||:|||||:|:|||||:|:|||||:|:|||||:|:|||||:|:|||||:|:|||||:|:
Db 115 IIPPTJADMGDTIETIVYKIKSKNGTSHHGHGKGTMLHDGANGITECPIPPKGRK 174
   ||:|||||:|:|||||:|:|||||:|:|||||:|:|||||:|:|||||:|:|||||:|:
OY 124 VYRFAKQOYGTSMYSHFSKQYGVGAIOINGPASPYPYDGLVPSIDYYSADDEL 183
   ||:|||||:|:|||||:|:|||||:|:|||||:|:|||||:|:|||||:|:|||||:|:
Db 175 VYRFAKQOYGTSMYSHFSKQYGVGAIOINGPASPYPYDGLVPSIDYYSADDEL 234
   ||:|||||:|:|||||:|:|||||:|:|||||:|:|||||:|:|||||:|:|||||:|:
OY 184 VELTKNSGAFSDNVLENGAKHPGEDEYANVTLPGRHRRLINTSVENHFOVSLV 243
   ||:|||||:|:|||||:|:|||||:|:|||||:|:|||||:|:|||||:|:|||||:|:
Db 235 VILTOHAGPPSPNNVLENGAKHPGEDEYANVTLPGRHRRLINTSVENHFOVSLV 294
   ||:|||||:|:|||||:|:|||||:|:|||||:|:|||||:|:|||||:|:|||||:|:
OY 244 NHTMCITADMPVNAVNTVDSLFLGVGORYDVVLEARNFGNTYFVFGGLCGGSRN 303
   ||:|||||:|:|||||:|:|||||:|:|||||:|:|||||:|:|||||:|:|||||:|:
Db 295 NHTMCITADMPVNAVNTVDSLFLGVGORYDVVLEARNFGNTYFVFGGLCGGSRN 354
   ||:|||||:|:|||||:|:|||||:|:|||||:|:|||||:|:|||||:|:|||||:|:
OY 304 PYPAIFHYAGRGPPDEGKAPVDHNCIDLPNLEKPVARADYPLSGFARADNTLDTL 363
   ||:|||||:|:|||||:|:|||||:|:|||||:|:|||||:|:|||||:|:|||||:|:
Db 355 KYPAIFRYOGAPKALPTNKGVAAPPDHQCIDLNDLKPVLRSLNTNSIALNTGNTIPITL 414
   ||:|||||:|:|||||:|:|||||:|:|||||:|:|||||:|:|||||:|:|||||:|:
OY 364 DTGTPLFVYKNGVSAINIDMGRAVYVYLTQNTSPFGNYIVVNGADQSVYLIENDP 423
   ||:|||||:|:|||||:|:|||||:|:|||||:|:|||||:|:|||||:|:|||||:|:
Db 415 DG----FVVRVNGTAININMKNRFLVETVMTGNTYSQSDNIYVBEVGNOMKRWYLIENDP 469
   ||:|||||:|:|||||:|:|||||:|:|||||:|:|||||:|:|||||:|:|||||:|:
OY 424 GAPTLPHPMLHGHDFYVLCRSPDESPASNERHVPFADAGLISGANVPRDVMPLA 483
   ||:|||||:|:|||||:|:|||||:|:|||||:|:|||||:|:|||||:|:|||||:|:
Db 470 DGAFSLPHPHHHDHDLILGRSPDYTAISQTRVFPDPAVDMALNNNNPRTPTALIPA 529
   ||:|||||:|:|||||:|:|||||:|:|||||:|:|||||:|:|||||:|:|||||:|:
OY 484 FGVVYLSFRADNCGAMLFCHIHAMHVSGLGVYVLEPADLRCGASDADDLRLCADW 543
   ||:|||||:|:|||||:|:|||||:|:|||||:|:|||||:|:|||||:|:|||||:|:
Db 530 KGMILLIFRDNPSWMLHCHIAMHVSGLSNOFLERADLRNLSISPADKKAFFNDNDAM 589
   ||:|||||:|:|||||:|:|||||:|:|||||:|:|||||:|:|||||:|:|||||:|:
OY 544 RRYWPTN-PYKPSDSGLK 560
   ||:|||||:|:|||||:|:|||||:|:|||||:|:|||||:|:|||||:|:|||||:|:
Db 590 RAYFPDNPAPPKDDSGLR 607
   ||:|||||:|:|||||:|:|||||:|:|||||:|:|||||:|:|||||:|:|||||:|:

```

```

CC 3 OR COUPLED BINOCULAR (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: Secreted (Potential).
CC -1- SIMILARITY: BELONGS TO THE FAMILY OF MULTICOPPER OXIDASES.
CC -1- SIMILARITY: CONTAINS 3 PLASTOCYANIN-LIKE DOMAINS.
CC -----
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CC -----
DR EMBL: M73257; AAA33105.1; -.
DR EMBL: S38903; AAA09235.1; -.
DR InterPro: IPR001117; Cu-oxidase.
DR InterPro: IPR002355; Multicopper oxidase2.
DR Pfam: PF00394; Cu-oxidase; 3.
DR PROSITE: PS00079; MULTICOPPER_OXIDASE1; 1.
DR PROSITE: PS00080; MULTICOPPER_OXIDASE2; 1.
KW Oxidoreductase; Signal; Copper; Metal-binding; Lignin degradation;
KW Glycoprotein; Repeat.
FT SIGNAL 1
FT CHAIN 21
FT DOMAIN 66
FT DOMAIN 198
FT DOMAIN 416
FT METAL 126
FT METAL 128
FT METAL 171
FT METAL 173
FT METAL 463
FT METAL 466
FT METAL 468
FT METAL 533
FT METAL 534
FT METAL 535
FT METAL 539
FT METAL 539
FT CARBOHYD 121
FT CARBOHYD 121
FT CARBOHYD 234
FT CARBOHYD 242
FT CARBOHYD 242
FT CARBOHYD 265
FT CARBOHYD 323
FT CARBOHYD 323
FT CARBOHYD 407
FT CARBOHYD 407
FT CARBOHYD 425
FT CARBOHYD 425
SO SEQUENCE 591 AA; 64696 MW; B2F44CB2AD77701 CRC64;

```

Query Match 58.5%; Score 1849; DB 1; Length 591;  
Best Local Similarity 59.9%; Pred. No. 3.3e-124;  
Matches 337; Conservative 74; Mismatches 144; Indels 8; Gaps 6;

```

OY 1 QOSCNFSPNRACMTDG-YDINTDYENDSPDGVVPTLTITLTDVNTGPGVYKEMVLYNNS 59
   ||:|||||:|:|||||:|:|||||:|:|||||:|:|||||:|:|||||:|:|||||:|:
Db 33 QPNCNTASNRACMTDG-YDINTDYENDSPDGVVPTLTITLTDVNTGPGVYKEMVLYNNS 92
   ||:|||||:|:|||||:|:|||||:|:|||||:|:|||||:|:|||||:|:|||||:|:
OY 60 VNNSIIPTTFADMGDTIOVYVNNLETNGTSHHGHGKGTMLHDGANGITECPIPPK 119
   ||:|||||:|:|||||:|:|||||:|:|||||:|:|||||:|:|||||:|:|||||:|:
Db 93 VNGNIIILPVIHAQMGDTISTVYVNNLETNGTSHHGHGKGTMLHDGANGITECPIPPK 152
   ||:|||||:|:|||||:|:|||||:|:|||||:|:|||||:|:|||||:|:|||||:|:
OY 120 GGRVYLFYKQOYGTSMYSHFSKQYGVGAIOINGPASPYPYDGLVPSIDYYSADDEL 179
   ||:|||||:|:|||||:|:|||||:|:|||||:|:|||||:|:|||||:|:|||||:|:
Db 153 GGSYTYFIHAYGTSMYSHFSKQYGVGAIOINGPASPYPYDGLVPSIDYYSADDEL 212
   ||:|||||:|:|||||:|:|||||:|:|||||:|:|||||:|:|||||:|:|||||:|:
OY 180 ADELVELTKNSGAFSDNVLENGAKHP-ENGGEYANVTLPGRHRRLINTSVENHFOVSLV 238
   ||:|||||:|:|||||:|:|||||:|:|||||:|:|||||:|:|||||:|:|||||:|:
Db 213 ADELVELTKNSGAFSDNVLENGAKHP-ENGGEYANVTLPGRHRRLINTSVENHFOVSLV 272
   ||:|||||:|:|||||:|:|||||:|:|||||:|:|||||:|:|||||:|:|||||:|:
OY 239 QVSLVNTMCITADMPVNAVNTVDSLFLGVGORYDVVLEARNFGNTYFVFGGLCGGSRN 298
   ||:|||||:|:|||||:|:|||||:|:|||||:|:|||||:|:|||||:|:|||||:|:
Db 273 QVSLVNTMCITADMPVNAVNTVDSLFLGVGORYDVVLEARNFGNTYFVFGGLCGGSRN 332
   ||:|||||:|:|||||:|:|||||:|:|||||:|:|||||:|:|||||:|:|||||:|:
OY 299 GGSNRPYPAIFHYAGRGPPDEGKAPVDHNCIDLPNLEKPVARADYPLSGFARADNT 358
   ||:|||||:|:|||||:|:|||||:|:|||||:|:|||||:|:|||||:|:|||||:|:

```



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CC -----
DR EMBL: Y08827; CAA70061.1; -
DR InterPro: IPR001117; Cu-oxidase.
DR InterPro: IPR002355; Multic_oxidase2.
DR Pfam: PF00394; Cu-oxidase; 3.
DR PROSITE: PS00079; MULTICOPPER_OXIDASE1; 1.
DR PROSITE: PS00080; MULTICOPPER_OXIDASE2; 1.
DR Oxidoreductase; Signal; Copper; Metal-binding; Glycoprotein; Repeat;
KM Lignin degradation; Melanin biosynthesis; Multigene family.
FT SIGNAL 1 23
FT PROPEP 24 48
FT CHAIN 49 605
FT PROPEP 606 621
FT DOMAIN 78 201
FT DOMAIN 210 367
FT DOMAIN 430 566
FT METAL 138 138
FT METAL 140 140
FT METAL 183 183
FT METAL 185 185
FT METAL 476 476
FT METAL 479 479
FT METAL 481 481
FT METAL 548 548
FT METAL 549 549
FT METAL 550 550
FT METAL 554 554
FT METAL ? ?
FT CARBOHD 133 133
FT CARBOHD 261 261
FT CARBOHD 276 276
FT CARBOHD 289 289
FT CARBOHD 325 325
FT CARBOHD 334 334
FT CARBOHD 401 401
FT CARBOHD 421 421
FT CARBOHD 441 441
SQ SEQUENCE 621 AA; 68129 MW; 79F85E2ED5C1CA7 CRC64;

Query Match 70.7%; Score 2231.5; DB 1; Length 621;
Best Local Similarity 68.9%; Pred. No. 2,1e-151;
Matches 397; Conservative 65; Mismatches 109; Indels 5; Gaps 4;

OY 1 QOSCTPSNRACWTDGDIINTDYEVSDPTGVRRPTLTLLEVDNMTGPDGVKVKMLV 60
DB 46 QSSCHTAARACWAPGDFDINTDYESTPMTGVRRPTLTLLEVDNMTGPDGVKVKMLV 105
OY 61 NNSIIGPTFEADMGDTIOVTVNNLTNGSTHMHGLHKGKNTLHGANGITRECPKPG 120
DB 106 NDIRESPTTANWDMIOVNVNINLTNGSTHMHGLHKGKNTLHGANGITRECPKPG 165
OY 121 GKRVRFAKQOYGTSMYHSFSAQYNGVGAIOINGPASPDPYDGLGVPISDYSSA 180
DB 166 GSRIVFRFRAQOYGTSMYHSFSAQYNGVGAIOINGPASPDPYDGLGVPISDYSSA 225
OY 181 DELVELTKNSGAPFSDNVLPNGTAKHPEEGEYANVTLPGRHRLRLINTSVENHFOY 240
DB 226 DVLVEETNMGPPSPDTVLFKGHKNPQTAGCFANVTLPGRHRLRLINTSVENHFOY 285
OY 241 SLVNHMCITADMVPMVPMATVDSLGLVGORADVITENRPPGVPWNTFGGGLCG 300
DB 286 KIONHTMTITADMVPMVPMATVDSLGLVGORADVITENRPPGVPWNTFGGGLCG 345
OY 301 SRNPYPALFHYAGAPGPTDEGKAPVDHNCIDLPNLPVAVADYPLSGFAKRAADNTLD 360
DB 346 SLNPHFAAVERGQAGVNTLPNTNIGTPAADANCDMLNLPVAVRSVPSTSGFPRPNTLP 405
OY 361 VILDTGTGLFVFKVNGSAINIDMGAAVVDYVLTQNTSPPGNINYEYNGAOWMSTWLE 420
DB 406 VSLTGTGLFVFKVNGSAINIDMGAAVVDYVLTQNTSPPGNINYEYNGAOWMSTWLE 465
OY 421 NDEGAFETLPHPMHLGHGFYVLRSPDESAS--NERHVFDPARAGLLSGANPVRDV 478
DB 585 NCNAMRAYMPTNPFRIDSLKVKWVGHPDMYIK 620

RESULT 2
ID LACL_NEUCR STANDARD; PRT; 619 AA.
AC P06811;
DT 01-JAN-1988 (Rel. 06, Created)
DT 01-JUL-1989 (Rel. 11, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Laccase precursor (EC 1.10.3.2) (Benzenediol: oxygen oxidoreductase)
DE (Urishiol oxidase) (Laccase allele OR).
GN LACC.
OS Neurospora crassa.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC Sordariales; Sordariaceae; Neurospora.
OX NCBI_Taxid=5141;
RN SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
RP MEDLINE=88087214; PubMed=2961749;
RA German U.A., Mueller G., Hunziker P.E., Lerch K.;
RT Characterization of two allelic forms of Neurospora crassa laccase.
RL Amino- and carboxyl-terminal processing of a precursor.
J. Biol. Chem. 263:885-896(1988).
[2]
RP SEQUENCE OF 379-619 FROM N.A.
RX MEDLINE=87067412; PubMed=2947240;
RA German U.A., Lerch K.;
RT Isolation and partial nucleotide sequence of the laccase gene from
RT Neurospora crassa: amino acid sequence homology of the protein to
RT human ceruloplasmin.
J. Proc. Natl. Acad. Sci. U.S.A. 83:8854-8858(1986).
RL - FUNCTION: LIGNIN DEGRADATION AND DETOXIFICATION OF LIGNIN-DERIVED
CC PRODUCTS (PROBABLE).
CC -1- CATALYTIC ACTIVITY: 4 benzenediol + O(2) -> 4 benzoquinone + 2
CC H(2)O.
CC -1- COFACTOR: BINDS 4 CU-IONS PER MOLECULE. THREE DISTINCT CU
CC CENTERS KNOWN AS TYPE 1 OR BLUE, TYPE 2 OR NORMAL, AND TYPE
CC 3 OR COUPLED BINUCLEAR (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: Secreted (Potential).
CC -1- SIMILARITY: BELONGS TO THE FAMILY OF MULTICOPPER OXIDASES.
CC -1- SIMILARITY: CONTAINS 3 PLASTOCYANIN-LIKE DOMAINS.
CC
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CC
DR EMBL: M14554; AAA33590.1; -
DR EMBL: M18333; AAA33591.1; -
DR PIR: A28523; KSNCLD.
DR PIR: A29762; A29762.
DR InterPro: IPR001117; Cu-oxidase.
DR InterPro: IPR002355; Multic_oxidase2.
DR Pfam: PF00394; Cu-oxidase; 3.
DR PROSITE: PS00079; MULTICOPPER_OXIDASE1; 1.
DR PROSITE: PS00080; MULTICOPPER_OXIDASE2; 1.
KW Oxidoreductase; Signal; Copper; Metal-binding; Lignin degradation;
KW Glycoprotein; Repeat.
FT SIGNAL 1 21
FT PROPEP 22 49
FT CHAIN 50 606
LACCASE.

```

## RESULT 14

S18746

laccase (EC 1.10.3.2) - basidiomycete (Phlebia radiata)

C:Species: Phlebia radiata

C:Date: 22-Nov-1993 #sequence, revision 10-Nov-1995 #text, change 11-Jun-1999

C:Accession: S18746

R:Salomon, M.; Miku-Pavola, M.L.; Knowles, J.K.C.

J. Gen. Microbiol. 137, 1537-1544, 1991

A:Title: Isolation and structural analysis of the laccase gene from the lignin-degrading

A:Reference number: S18746; MUID:92055223; PMID:1955850

A:Accession: S18746

A:Molecule type: DNA

A:Residues: 1-548 &lt;S&gt;L&gt;

A:Cross-references: EMBL:X52134; MID:93257; PIDN:CAA36379.1; PID:93258

C:Genetics:

A:Insertions: 61/3; 84/3; 125/1; 163/1; 184/2; 217/2; 269/3; 336/3; 355/3

C:Superfamily: laccase

C:Keywords: oxidoreductase

## Query Match

Best Local Similarity

Matches 162; Conservative 66; Mismatches 195; Indels 90; Gaps 22;

17.6%; Score 556; DB 2; Length 548;

Pred. No. 6e-33;

Matches 162; Conservative 66; Mismatches 195; Indels 90; Gaps 22;

QY 49 PDGVYKRWLVNNSITGPTIFADMGDTIQVTVNNLETNG-----TSIHMGHLHQGTN 103  
 DB 38 PDGFSRQAV-LAEGVFPGLIAGNKGDNFQINVIDEL-TNATMLKTTTHMHGFFQHGNT 95  
 C:Accession: S18746

QY 104 LHDGANGTECPPIPKGGRKRYRKA-QQVGTSMYSHSFOYNGVYGATQINGPASP 162  
 DB 96 WADSPATINQCP-ASGDSFLYNQVDPQACTFWYHSLSTQYCDGLRGPVYVDPAD-P 153  
 C:Accession: S18746

QY 163 Y-----DTDLGVPPISDYYSNADELVELTKNSGAPF--SDNYLFGNTAKHPETG--EG 212  
 DB 154 YLDQYDODDSTVITLADWYHTAA-----RLGSPRPADTLTLINGLRCGEGAGCVS 205  
 C:Accession: S18746

QY 213 EXANVTLPGRHRLINTSVENHFOVSLVNHMCITADMVNANTVDSLGVGQR 272  
 DB 206 DLAVISYTKGRKRYRFLVSIQDSFFTSIDGHSIMLVENDATNHOPLTVDLITVIGOR 265  
 C:Accession: S18746

QY 273 YDVVIEANRFPNGYFWNTFFGGILCG--GSRNPYPALIFHYAGAP--GGPPTDEGKAPVD 329  
 DB 266 YSFLITLADQDDVNWIRANPGIGITTGPAAGIN---SAILRYDADADVETPTTQATSVY- 321  
 C:Accession: S18746

QY 330 HNCIDLPLKRVAVADVPVLSGFARADNTLDVTLDTGTPLTFVKKVNGSALINIDGRAV 389  
 DB 322 --VLSSENLAPLTNAAPGLPEVGVLDLALNFNLTFDG--PELKFQINGV----- 367  
 C:Accession: S18746

QY 390 DYVLTQMTSPPGYNIV--EVNGADQMS-----YWLLEND-----PGAPFTLPHRM 433  
 DB 368 -----TFVPPYVPLIQIISGAOSADLLPSGSVYALPSNATTELSPFAGALGGRHPF 420  
 C:Accession: S18746

QY 434 HLHGDEYVLRSPDESASNERHVPDPADAGLLSGANPFRDVSMLPAG--WVLSFR 492  
 DB 421 HLHGTFSSV-----RPAGSTTYNY-----VNPQRDVYSIGNGDMVTIRFD 463  
 C:Accession: S18746

QY 493 ADNGCANLFRCHTAMWYSGLGVYTLERADDLR 525  
 DB 464 TNNGPWFHLCHIDMHLAALPLSLRTSLTLR 496  
 C:Accession: S18746

## RESULT 15

T05020

L-ascorbate oxidase (EC 1.10.3.3) - Arabidopsis thaliana

N:Alternate names: protein T19p19.220

C:Species: Arabidopsis thaliana (mouse-ear cross)

C:Date: 23-Apr-1999 #sequence, revision 23-Apr-1999 #text, change 16-Jul-1999

C:Accession: T05020

R:Bevan, M.; Montfort, A.; Casacuberta, E.; Puidomenech, P.; Hohelsel, J.; Mewes, H.W.;

submitted to the Protein Sequence Database, April 1998

A:Reference number: Z15394

A:Accession: T05020

A:Molecule type: DNA

A:Residues: 1-582 &lt;BRV&gt;

A:Cross-references: EMBL:AL022605

A:Experimental source: cultivar Columbia; BAC clone T19P19

C:Genetics:

A:Map position: 4

A:Insertions: 98/3; 129/3; 200/3; 265/3

A:Note: T19P19.220

C:Superfamily: laccase

C:Keywords: oxidoreductase

F:381-577/Domain: carboxyl-terminal beta-barrel #status predicted &lt;BB3&gt;

F:51-234/Disulfide bonds: #status predicted

F:92,486/Binding site: copper (His) (type 2) #status predicted

F:94,136,138,488,545,547/Binding site: 2Cu-O cluster (His) (copper type 3) #status f

F:113-577/Disulfide bonds: #status predicted

F:195,398,481,551/Binding site: substrate (Trp, Trp, Glu, His) #status predicted

Query Match 17.3%; Score 547.5; DB 2; Length 582;

Best Local Similarity 25.9%; Pred. No. 2.8e-32;

Matches 157; Conservative 91; Mismatches 215; Indels 143; Gaps 21;

QY 4 CNTPSNRACWTDGYDINDYEDSPDTGVVRYPLTLTEVDNMTPDGVYKRYLVNNS 63  
 DB 31 CQGIKRRFKW-----EYKIEFKSPD-----CEKLVITTINGK 62  
 C:Accession: S18746

QY 64 IIGPTIFADMGDTIQVTVNNLETNGTSIHMGHLHQGTNMLHDGANGTECPPIPKGGR 123  
 DB 63 FPGPTIKAQOGDTLVLELKNSEFMENAVAHMHGIRQICTPMDGVEGVQCPILP-GEVF 121  
 C:Accession: S18746

QY 124 VYRKAQOYGTSMYSHSFOYNGVYGATQINGPASP----YDVLGVPPISDYYS 179  
 DB 122 YQFVYVPRPGTYMHSYHGQRESGLIGMTQVSPATEPEFTYDYRN-FLTLDMYHKS 180  
 C:Accession: S18746

QY 180 ADELVELTKNSGAPFS-----DNVLFNGTAKH-----PETGEGERANY----- 217  
 DB 181 MSE--KATGLASIPFKWVGEPQSLMIGRGFRNCSNLTTPPLSYSCVSNADCSRFT 238  
 C:Accession: S18746

QY 218 -TLTPGRHRLRLINTSVENHFOVSLVNHMCITADMVNANTVDSLGVGQR 276  
 DB 239 LTVIPGKTYRLRLISLALSLALSFQIGHNLTVLEADGHVPEPTVKNLEFVSGEFTSVL 298  
 C:Accession: S18746

QY 277 IEANRFP-GNVWFVTEGGGILCGSRNPYPALIFHYAGAP--GGPPTDEGKAPVD 334  
 DB 299 LKADQNRNRNWTSSI---VSRPATTPPATVAVNYTPNHRRRRPPTSESS----- 346  
 C:Accession: S18746

QY 335 LPNLKP-----VVARVPLSGFARADNTLDVTLDTGTPLTFVKKVNGSALINIDGRAV 389  
 DB 347 --NIVPEMNDPRLSLAQSIAIKARGFTHALPENSDEVIL-VLNTQN-----EVNGYRR 397  
 C:Accession: S18746

QY 378 -SAINIDGRAVDYV--LQNTSFPFGYNIVVEYNGADQMSYMLI----- 419  
 DB 398 WSVNNSVYHHPKPTLYLALQNLNAPDMRFTAPENDYSRNYDIFAPPLANATTSQGIY 457  
 C:Accession: S18746

QY 420 -----ENDPGAPFTLPHRMHLHGDFUYLGRSPDESASNERHVPDPAD 465  
 DB 458 RLNRNSTVDVILQANANNNANNNSTHVMHLHGDFVVLGIGEGK-----PNESEDP 508  
 C:Accession: S18746

QY 466 GLLSGANPVRDVSMLPAGFVYVLSFRADNPGANLFRCHTAMWYSGLGVY---LERAD 522  
 DB 509 KRYNRVDPPIKKNVAVQVPGWTLALFRADNPGVMSFCHIESHFQMGYIFESGIDKYS 568  
 C:Accession: S18746

QY 523 DLRCAY 528  
 DB 569 SLPSI 574  
 C:Accession: S18746

Search completed: December 4, 2002, 10:46:54  
 Job time: 24 secs



Db 144 PFVVYDNDPHASLYDVNDNDFVITTLADWHTAA-----KLGPAPFLGADATLNGL 195

QY AKHPEGESEYANTLTGRRHRLRLINTSEVNHFOYSLVHTMCTIADAVPVNAMYD 263

Db 196 GRSSTTAADLAIVNTKGRKRYRRLVSLSCDPMHTSISDHDTLIEVDINSQPLVVD 255

QY 264 SLFLVGORVDVIEANRTPGNYWF--NWTFGGILCGSRNPYPALIFHAGAPGPP 321

Db 256 SIQFAORSEFVLNADODVGNWYIRANPNNGVAFAGIN-----SALIRDGDAPVEPT 311

QY 322 DEGAAPVDHNCIDLPNKFPVYARVPLSGFRKRDNTLDLTGTGPLEYWKVNGSAT- 380

Db 312 TGTQTPP--KPLANEVDLHPPLATMAVPGSPVAGVDTAINMAFNNGTFF--TNGASFV 366

QY 381--NIDMGRAVDVYL/TONTSPFG--YNIYEVNGADQMSWLIENDGAPFLPRLPHH 436

Db 367 PPIYVYLQITISGANOADLLPGSVYSLPS--NADIEISFATPAARQA-----PHEPLH 421

QY 437 GHDFYVLGRSPDES PASNERHVPDPADAG--LISGANPVYRDY--SMLPAFG--WVYLSF 491

Db 422 GHAFAYV-----RSAGSTVYNYNDPIPROVYSTGTPAAGDNTIRF 462

QY 492 RADPGAMLFCHITAMHVSGLGVYLERADDLFGAVSDADADDLRLCADMKRYPTNP 551

Db 463 RTDNPGEWFLCHIDFHEAGFAVFAEDIPDVASA-----NP 500

QY 552 YPKSDSGL 559

Db 501 VPQWMSDL 508

## RESULT 6

S68120  
Laccase (EC 1.10.3.2) 4 precursor - Rhizoctonia solani

C:Species: Rhizoctonia solani

C:Date: 19-Mar-1997 #sequence\_revision 19-Mar-1997 #text\_change 20-Jun-2000

C:Accession: S68120; S77976; S72364

R:Wahlthner, J.A.; Xu, F.; Brown, K.M.; Brown, S.H.; Gollightly, E.J.; Halkier, T.; Kai

Curr. Genet. 29, 395-403, 1996

A:Title: The identification and characterization of four laccases from the plant pathoge

A:Reference number: S68117; MUID:9611523; PMID:8598061

A:Accession: S68120

A:Molecule type: DNA

A:Residues: 1-529 <MANH>

A:Accession: S77976

A:Molecule type: protein

A:Residues: 20-53;132-180;203-217;378-396;440-465;489-513;520-529 <MAN2>

R:Wahlthner, J.A.

submitted to the EMBL Data Library, September 1995

A:Reference number: S72364

A:Accession: S72364

A:Molecule type: DNA

A:Residues: 1-417, 'CAOHRH', 424-469, 'A', 471-483, 'CT', 484, 'R', 486, 'GSH', 490, 'S', 492, 'PRPP',

A:Cross-references: EMBL:Z54277; NID:g1150567; PIDN:CA91042.1; PID:g1150568

C:Genetics:

A:Gene: lcc4

A:Insertions: 56/3; 70/3; 82/3; 87/3; 101/1; 126/2; 143/1; 147/1; 170/2; 193/2; 250/3; 276/

C:Superfamily: laccase

C:Keywords: copper; oxidoreductase

F:1-19/Domain: signal sequence #status predicted <SIG>

F:20-59/Product: laccase 4 #status experimental <MAN>

Query Match 19.4%; Score 612.5; DB 2; Length 529;

Best Local Similarity 30.6%; Pred. No. 4.1e-37;

Matches 175; Conservative 73; Mismatches 202; Indels 121; Gaps 24;

25 VDSPDGCVNRYTLTLEVEVNMGTGPGVVEKVLVNSIIGPTIFADMGDTIOVYINN 84

Db 14 VSPFAFAVNNYKFDINNVN--VAPDS--FQRPVSVNGVLGTLTANKDITLRINVT 70

QY 85 LE-----TNGTSIHMHGILHOKGTNLHDGANGITECPIPKGRKRYRKAQ---OQYGSWY 137

Db 71 LTDPMSMRATTIHHGILFQATTADEDSGPAFYTCPI---AONLSYTEIFELHOGTGMWY 127

QY 138 HSHESAQYNGVGAIOI-----NGPASLDPDND--LGFPISDYXSSADELVE---LTKN 189

Db 128 HAHLASQYVGLKRPDLTYDPNDPKSRDYDDASTVWMLIEDWYHTTPVPLEKQMFSTNN 187

QY 190 SG--APFSDNVLEFNGTAKHPEGESEYANTLTG-----GRRHRLRLINTSEVNHFO 239

Db 188 TALLSPVDSGLIN-----GKGRVVGGRVAVRSYINVKRGRYRLRYINMASAISFT 239

QY 240 VSLVNTMCTIADMPVNMATYDLSFLVGQRYDVYIEANRTPGNTWFN--VTFGGGL 297

Db 240 FSIEGRLVTEADGIPHPLVDSFOIYAGQRSYVIEANQFANWIRAPMTVAG--- 296

QY 298 CGGSRNPRPA--AIFHAGAPGPPDE-----GKAPVDHNCIDLN----- 337

Db 297 AGTIANADPTNVRVAVLHTEGAPNAEPTEGSAIGTALVEENHALINPGAPGSSAPADV 356

QY 338 -LKPVVAROVPLSGFARADNTLDVLTGTGPLEYWKVNGSAINIDMGRAVDVYLTON 396

Db 357 SIMLAIGRST--VDGILAFTEFNNTKYEAPSLPTLLKILANNAS-----NDADFTNEH 407

QY 397 TSFPPGYNIVEVN---GADQMSWLIENDGAPFTLPHMHLGHDFYV--LGRSPDES 450

Db 408 TIVLPNKKYIELNTIGAD-----HPILHGHVFDIVKSLGCTPNY- 448

QY 451 PASNERHVPDPADAGLLSGANPVYRDVSMLPAGVYVLSFRADNPGAMLFCHIAMHVS 510

Db 449-----VNPPRDVYRVGGTG--VLLRFTKTDNPGPWFVCHIDWHLE 487

QY 511 GGLGVYLERADDLFGAVSDADADDL--DRLC 540

Db 488 AGLALVEAEAPSOIRQGVQSVOPNNANQLC 518

## RESULT 7

JC3536  
Laccase (EC 1.10.3.2) 4 precursor - white-rot fungus (Trametes villosa)

N:Alternate names: urushiol oxidase

C:Species: Trametes villosa (white-rot basidiomycete)

C:Date: 28-May-1997 #sequence\_revision 18-Jul-1997 #text\_change 19-May-2000

C:Accession: JC3536

R:Yaver, D.S.; Gollightly, E.J.

Gene 181, 95-102, 1996

A:Title: Cloning and characterization of three laccase genes from the white-rot bas

A:Reference number: JC3535; MUID:97128774; PMID:8673314

A:Accession: JC3536

A:Molecule type: DNA

A:Residues: 1-520 <YAV>

A:Cross-references: GB:U78077; NID:g1322078; PIDN:AB47734.1; PID:g1322079

C:Comment: This enzyme is a multi-copper enzyme which catalyzes the oxidation of phe

C:Genetics:

A:Gene: lcc4

A:Insertions: 62/3; 85/3; 126/1; 185/2; 217/2; 269/3; 335/3; 424/3; 463/3; 503/1

C:Superfamily: laccase

C:Keywords: oxidoreductase

F:1-22/Domain: signal sequence #status predicted <SIG>

F:23-520/Product: laccase 4 #status predicted <MAN>

Query Match 19.1%; Score 603; DB 2; Length 520;

Best Local Similarity 32.2%; Pred. No. 2e-36;

Matches 180; Conservative 76; Mismatches 211; Indels 92; Gaps 24;

30 TGVVRYPT-LTLEVEVNMGTGPGVVEKVLVNSIIGPTIFADMGDTIOVYINN--E 86

Db 21 SAALGPTDLTISNGD--VSPDSFTRAAY--LANGVPPGLITGNKGNPQINVIDNLSNE 77

QY 87 T--NGTSIHMHGILHOKGTNLHDGANGITECPIPKGRKRYRKAQ---OQYGSWYHSHFSA 143

Db 78 TMLKSTSIHHGFFQKGTNADGAFAVNCPI--ATGNSFLYDFTADQAGTFYHSHLSF 136

QY 144 QYNGVYVGAIOINGRPSLPI-----DTDLGVPISDIYXSSADELVELTKNSGAPF--- 194

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Db 226 DVAEEFMNGPPSPDVLKFKHGKKNPOTGAKFAMVTLTPGKRRRLRLINTSTHDFQL 285
QY 241 SLVNHPCIIAADMVPMNAMVDSLFLGVGORVYVTEANTPGWYMNPPFGGLCGG 300
Db 286 KLONHHTITIAADVPVQAOQVDSLFLAVGORYVTIDANKSVGNNAFPGGLACGA 345
QY 301 SRNPYPAIFHYAGAPGPTDEGKAPVDHNCIDLPLMLKPVAVDPLSGFAKRAADNTLD 360
Db 346 SLNPHPAAYRYOGAPRTLPNTIGTPADANCMNLNLTPLVSRSVPTSGTTPRNMTLP 405
QY 361 VTLDTGTPLFVWKVNGSAINIDMGRAVDVLTQNTSPFPGYIVVEVNGADQSWYLIE 420
Db 406 VSLTIGTPTPLFVWKVNGSAINIDMKRPIVDVIAQNTSYPPQAVVITVNSVQMTYMLIE 465
QY 421 NDGAPPTLPHMHLHGHDVYLGRSPDESASP--NEHVPDPARADGLSGANPVRDY 478
Db 466 NDPTGPPSIFHPMHLHGHDVYLGRSPDQ--PAGVPQTRRPNPATDMLKSSNPRRDV 524
QY 479 SMLPFGWVYLSPRADNGAMLFCHITAMHVSGLGVYTLERADDLRGAVSDADADLDR 538
Db 525 AMLPANGLMILIAFKSDNRGAMLFCHITAMHVSGLSVQYLERPDRLNRGFSQADKQHN 584
QY 539 LCAWMRYPTNPPKDSGLK-HRWV-EEGEMLVK 572
Db 585 NCMNARWYPTNPPKIDSGLKVKWGEHPDNYIK 620

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## RESULT 2

laccase (EC 1.10.3.2) precursor - Neurospora crassa (strain OR)

N:Alternate names: urishiol oxidase

C:Species: Neurospora crassa

C>Date: 30-Sep-1991 #sequence\_revision 30-Sep-1991 #text\_change 11-Jun-1999

C:Accession: A28523; A29762

R:Germann, U.A.; Mueller, G.; Hunziker, P.E.; Lerch, K.

J. Biol. Chem. 263, 885-896, 1988

A:Title: Characterization of two allelic forms of Neurospora crassa laccase. Amino- and

A:Reference number: A28523; PMID:88087214; PMID:2961749

A:Accession: A28523

A:Molecule type: DNA

A:Residues: 1-619 <GER>

A:Cross-references: EMBL:M14554

R:Germann, U.A.; Lerch, K.

Proc. Natl. Acad. Sci. U.S.A. 83, 8854-8858, 1986

A:Title: Isolation and partial nucleotide sequence of the laccase gene from Neurospora

A:Reference number: A29762; MIMD:87067412; PMID:2947240

A:Accession: A29762

A:Molecule type: DNA

A:Residues: 379-619 <GE2>

A:Cross-references: GB:M14554; NID:q168823; PIDN:AAA33590.1; PID:q168824

C:Comment: This enzyme, which catalyzes the oxidation of benzendiol to benzosemiquinone

C:Genetics: 86/3

A:Introns: 86/3

C:Superfamily: laccase

C:Keywords: copper; glycoprotein; oxidoreductase

F:1-21/Domain: signal sequence #status predicted <SIG>

F:22-49/Domain: propeptide #status predicted <PRO>

F:50-619/Product: laccase #status predicted <MAT>

F:84-215/Domain: amino-terminal beta-barrel #status predicted <BB1>

F:216-372/Domain: middle beta-barrel #status predicted <BB2>

F:331-580/Domain: carboxyl-terminal beta-barrel #status predicted <BB3>

F:139,282,295,340,422,444/Binding site: carboxylate (Asn) (covalent) #status predicted

F:144,480/Binding site: copper (His) (type 2) #status predicted

F:146,189,191,482,548,550/Binding site: 2Cu-0 cluster (His) (type 1) #status predicted

F:477,549,554/Binding site: copper (His, Cys, His) (type 1) #status predicted

Query Match 64.3%; Score 2032; DB 1; Length 619;  
Best Local Similarity 64.3%; Pred. No. 3,4e-141;  
Matches 359; Conservative 80; Mismatches 113; Indels 6; Gaps 2;

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Db 55 CNSPTNRCWSPGFNINTDYELGTPNTGKTRRYKLLTETDNWIGDGVIRKQVAVNDK 114
QY 64 IISPTIPADMGDDTIQVYINNLFTNGTISIHWHGLOKGTNLHOCANGTECPPIPKGRK 123
Db 115 IIGPTIQADMGDYLETIYINLTKSNGTISIHWHGLOKGTNLHOCANGTECPPIPKGRK 174
QY 124 VYRKAQOYGTSMYSHFSASOYNGVGAIOINCPASLPYTDGLGVPFISPYSSADEL 183
Db 175 VYRKAQOYGTSMYSHFSASOYNGVGAIOINCPASLPYTDGLGVPFISPYSSADEL 234
QY 184 VELTKNSGAPPSDVLNENGAKHPEETGEGEYANTLPGRRRRLRLINTSYENHFOVSLV 243
Db 235 VLTQOHAGPPSPSNVTLFNGFAKHPTTGAGYATVSLFGKRRRLRLINTSYENHFOVSLV 294
QY 244 NHTMCIIAADMVPMNAMVDSLFLGVGORVYVTEANTPGWYMNPPFGGLCGGSRN 303
Db 295 NHTMTIISADLVPOQYVDSLFLVGORYVTIIDAMQAVGNVFNWYFNGSKLGGSDN 354
QY 304 PYPAIFHYAGAPGPTDEGKAPVDHNCIDLPLMLKPVAVDPLSGFAKRAADNTLDVTL 363
Db 355 HYPAIRRYOGAPKALPTNGAVAVDHQCIDLNLKPLVQSLMTVNGTITPTL 414
QY 364 DTGTPLFVWKVNGSAINIDMGRAVDVLTQNTSPFPGYIVVEVNGADQSWYLIE 423
Db 415 DG-----FVWVRNGTAININMKPYLEVLTGNTNYSQSDNIYQEGVQMKWYLIE 469
QY 424 GAPPTLPHMHLHGHDVYLGRSPDESASPNERHVPDPARADGLSGANPVRDY 483
Db 470 DGAFTSLPHMHLHGHDVYLGRSPDVTAISQTRVFPDPAVMARLNGNPPRTAMLP 529
QY 484 FGWVLSFRADNPGAMLFCHITAMHVSGLGVYTLERADDLRGAVSDADADLRLCADW 543
Db 530 KGWILLIAFRDTPSPWMLHCHITAMHVSGLSNGFLERAQDLRNSIPADKKAFFNDQDAW 589
QY 544 RRYPTN-PPKDSGLK 560
Db 590 RAYFPDPAFPKDDSGLK 607

```

## RESULT 3

laccase (EC 1.10.3.2) precursor - Neurospora crassa (strain TS)

N:Alternate names: urishiol oxidase

C:Species: Neurospora crassa

C>Date: 30-Sep-1991 #sequence\_revision 30-Sep-1991 #text\_change 11-Jun-1999

C:Accession: B28523

R:Germann, U.A.; Mueller, G.; Hunziker, P.E.; Lerch, K.

J. Biol. Chem. 263, 885-896, 1988

A:Title: Characterization of two allelic forms of Neurospora crassa laccase. Amino-

A:Reference number: A28523; MIMD:88087214; PMID:2961749

A:Accession: B28523

A:Molecule type: DNA

A:Residues: 1-619 <GER>

A:Cross-references: EMBL:M18334; NID:q168827; PIDN:AAA33592.1; PID:q168828

C:Comment: This enzyme, which catalyzes the oxidation of benzendiol to benzosemiquinone

C:Genetics: 86/3

A:Introns: 86/3

C:Superfamily: laccase

C:Keywords: copper; glycoprotein; oxidoreductase

F:1-21/Domain: signal sequence #status predicted <SIG>

F:22-49/Domain: propeptide #status predicted <PRO>

F:50-619/Product: laccase #status predicted <MAT>

F:84-215/Domain: amino-terminal beta-barrel #status predicted <BB1>

F:216-372/Domain: middle beta-barrel #status predicted <BB2>

F:331,282,295,340,422,444/Binding site: carboxylate (Asn) (covalent) #status predicted

F:144,480/Binding site: copper (His) (type 2) #status predicted

F:146,189,191,482,548,550/Binding site: 2Cu-0 cluster (His) (type 1) #status predicted

F:477,549,554/Binding site: copper (His, Cys, His) (type 1) #status predicted

Query Match 64.0%; Score 2021; DB 1; Length 619;  
Best Local Similarity 63.8%; Pred. No. 2.2e-140;  
Matches 356; Conservative 83; Mismatches 113; Indels 6; Gaps 2;

Wed Dec 4 15:07:58 2002

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Page 10

[illegible]

Search completed: December 4, 2002, 10:51:23  
Job time : 14 secs

QY 171 PISDIYSSADELY--ELTKNSG-APESDNYLFNGTA--KHPEGEGETYANVTLPGRH 225  
 DB 163 IILGEMKSDIRAVONERFLGNGDANVSDAFLINGOPDILPCSRSDTY-MLTYESGKTY 221  
 QY 226 RLRLINTSVENHFPVSLVNHMTCILADNMVNMATVDSLFLVGQRIDVYIEANRTPN 285  
 DB 222 LIRMINAVMTIMEFSLANHSVTVGSDAATKPLKSDYITISGOTIDFLAQNTPSH 281  
 QY 286 YMFVNTGGGILCGSRNPYPALFHYAG--APGCP----- 319  
 DB 282 YV--MAARAFAVAGNPNMTTITAIIRKGNATASPSFPMPLPGENDTASVNTYILRS 339  
 QY 320 -----PTDEGKAPVDH-----NCIDLPN-----LKPVVA--- 343  
 DB 340 LGNKNYEVDVPEKNTDKLLEFPSINLPCPNNSCAGPENEFASVNNITFVPTIALQ 399  
 QY 344 -----RDVPLSGPAKADNTLDVTLDTGTPPLVWK-VNGSAINIDGRAVVDVLTQN 396  
 DB 400 AYYORINNYVSNPNPSPFENYTSDF--IPRDLMPQNETEVKVLKYNSTVEIVE-OG 456  
 QY 397 TSFPPGYNIVEVNGADQMSYMLIENDGAPFTLPHMHLGHDFYVIGRSPDESASNER 456  
 DB 457 TNLAG-----IDHPIHLHGOSFTYVWG-----LGNFN 485  
 QY 457 HVDPADAGILSGANPYRDVSMPLPAFGVVLSPRADNPGAMLFCHIAMHVSGLGV 516  
 DB 486 NATDPLN-----YNLVDPLMNTIAVPVSGWAVAFKASNPQVWLHCHLEHRLSMGDMV 541  
 QY 517 YL 518  
 DB 542 FI 543

## RESULT 12

US-09-942-185-2  
 ; Sequence 2, Application US/09942185  
 ; Patent No. US20020165113A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Aehle, Wolfgang  
 ; APPLICANT: Convents, Daniel  
 ; APPLICANT: Doornink, Monique  
 ; APPLICANT: van Gastel, Frans  
 ; APPLICANT: Rodrigues, Ana  
 ; APPLICANT: Topozada, Amr  
 ; APPLICANT: De Vries, Cornelis Hendrikus  
 ; APPLICANT: Wang, Huaming  
 ; TITLE OF INVENTION: Detergent Compositions Comprising No. US20020165113A1el Phenol O  
 ; FILE REFERENCE: C7567  
 ; CURRENT APPLICATION NUMBER: US/09/942,185  
 ; CURRENT FILING DATE: 2001-08-29  
 ; NUMBER OF SEQ ID NOS: 8  
 ; SOFTWARE: FastSeq for Windows Version 4.0  
 ; SEQ ID NO 2  
 ; LENGTH: 583  
 ; TYPE: PRT  
 ; ORGANISM: Stachybotrys chartarum  
 US-09-942-185-2

Query Match 7.6%; Score 241; DB 9; Length 583;  
 Best Local Similarity 25.0%; Pred. No. 9.8e-13;  
 Matches 152; Conservative 59; Mismatches 226; Indels 170; Gaps 32;

QY 25 VDSPTG-----VVRPYTLTL--TEVDNMTGPGGVKEMKLVNNSIIGPTIFADW 73  
 DB 66 VPNNTGEDILYEMERFESHQIYPLDEPANMVGDMSP-----GPTIIVPR 114  
 QY 74 GDTIQVYVNNLE-TNGSTIMHGLHOKGTLHGCANGITCPTIPKGRVYVFKAOY 132  
 DB 115 GTESVAFVNSGENTSPSVLHGSFSRAP--FDGMAEDTQP-----GEKKDYYPNRQA 168  
 QY 133 GTS-WYHSH-FSAOYGN--GVVGAIOINGPA--SLPYDIDLGAVFPISDIYSSADELYE 185

DB 169 ARMLYHDHAMSITAENAYMGAGVYMIODPAEDALNLPSCYGEEDI-----PLVL 219  
 QY 186 LTKNSGAFESDNYLFNGTAKHPEGE-----GEYANVTLP-----GRHRRLINTS 233  
 DB 220 TAKRYNA--DGTLP-----TNGEVSSEFWGDYIYVNGOPMPLMNOQPRKTRFRFLNAA 270  
 QY 234 VENHFOVSLVNH-----TWCIILAD--MVVNAMATVDSLFLVGQRIDVYIEANRT 282  
 DB 271 VSRFALYLTASEDESETRLPQVYIADOGGLEGYVD--PTLVIISMERREVIDS-- 325  
 QY 283 PGNTFVNTFEGGILCGSRNPYPALFHYAGA-----PGPPTDEGKAPVDHNCIDL 336  
 DB 326 -----TFAGOSI-----DIRMLPGAAGLGVEPEFDWTDKVMRFVDEVELESP 367  
 QY 337 NLKPVVA--RDVPL--SGFAKADNTLDVTLDTGTPPLVWKVNGSAINIDGRAVVDYV 392  
 DB 368 DTSEVPANLRDVPPEEGNMDPAPPTDDET--TGRANGQMTINGVTF-----SDVENR 420  
 QY 393 LTONTSEPPGYNIVEVNGADQMSYMLIENDGAPFTLPHMHLGHDFYVIGRSPDES 452  
 DB 421 LLRNV-----RDVPEIMRLNNSNG--WTHPVHILVDPERVLSRSTARG-- 463  
 QY 453 SNERHVEDPADAGILSGANPYRDVSMPLPAFGVVLSPRADNPGAMLFCHIAMH---- 508  
 DB 464 -----VEPYEAGILKDVWMLAREVYVEA-----HYAPFGVYMLHCHNLIHEDHD 510  
 QY 509 -----VSGGLGVYTLERAD-----LRGAVSDADADDRLCADMRRTYPT- 549  
 DB 511 MAAFNVTYLGADYINTTEFIDPMEPLMRPRPFIILGEPENSGSPSELATDRIOENASF 570  
 QY 550 NPYPKSD 556  
 DB 571 NPYAQAD 577

## RESULT 13

US-09-942-185-4  
 ; Sequence 4, Application US/09942185  
 ; Patent No. US20020165113A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Aehle, Wolfgang  
 ; APPLICANT: Convents, Daniel  
 ; APPLICANT: Doornink, Monique  
 ; APPLICANT: van Gastel, Frans  
 ; APPLICANT: Rodrigues, Ana  
 ; APPLICANT: Topozada, Amr  
 ; APPLICANT: De Vries, Cornelis Hendrikus  
 ; APPLICANT: Wang, Huaming  
 ; TITLE OF INVENTION: Detergent Compositions Comprising No. US20020165113A1el Phenc  
 ; FILE REFERENCE: C7567  
 ; CURRENT APPLICATION NUMBER: US/09/942,185  
 ; CURRENT FILING DATE: 2001-08-29  
 ; NUMBER OF SEQ ID NOS: 8  
 ; SOFTWARE: FastSeq for Windows Version 4.0  
 ; SEQ ID NO 4  
 ; LENGTH: 572  
 ; TYPE: PRT  
 ; ORGANISM: Myrothecium verucaria  
 US-09-942-185-4

Query Match 6.5%; Score 204; DB 9; Length 572;  
 Best Local Similarity 23.4%; Pred. No. 1.3e-09;  
 Matches 138; Conservative 68; Mismatches 233; Indels 150; Gaps 32;

QY 23 YEVDSPDTGVVRYPT-----LTLTEVDNMTGPGGVKEMKLVNNSIIGPTIFADWGTIQ 78  
 DB 77 YEVE-----IKPETHOYVPLDGSAD-LVGTGDSKSP-----GPTFQVPRGYEYV 118  
 QY 79 VTVINNLNETNGTSHMHGLHOKGTLHLDG-ANGITTECPIPKGRKRYVRFKAOYGTSMY 137  
 DB 119 VRFINNAEA-PNSVHLHGSFSRAA--FDGMAEDITE--PGSKDYIYFNRQSARTLYT 171  
 QY 138 HS---HFSAOYG-NGVVGAIQINGPA--SLPYDIDLGAVFPI-----SDIYSSADELYELT 187

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? TITLE OF INVENTION: LACCASE MUTANTS
? NUMBER OF SEQUENCES: 10
? CORRESPONDENCE ADDRESS:
? ADDRESSEE: No. US20010031490A1o No. US20010031490A1disk of No. US20010031490A1ch
? STREET: 405 Lexington Avenue
? CITY: New York
? STATE: NY
? COUNTRY: USA
? ZIP: 10174
? COMPUTER READABLE FORM:
? MEDIUM TYPE: Diskette
? COMPUTER: IBM Compatible
? OPERATING SYSTEM: DOS
? SOFTWARE: FASTSEQ for Windows Version 2.0
? CURRENT APPLICATION DATA:
? APPLICATION NUMBER: US/09/732,350
? FILING DATE:
? CLASSIFICATION:
? PRIOR APPLICATION DATA:
? APPLICATION NUMBER: 09/032,315
? FILING DATE:
? ATTORNEY/AGENT INFORMATION:
? NAME: Rozek, Carol
? REGISTRATION NUMBER: 36,993
? REFERENCE/DOCKET NUMBER: 5200.200-US
? TELECOMMUNICATION INFORMATION:
? TELEPHONE: 212-867-0123
? TELEFAX: 212-878-9655
? INFORMATION FOR SEQ. ID NO: 8:
? SEQUENCE CHARACTERISTICS:
? LENGTH: 575 amino acids
? TYPE: amino acid
? STRANDEDNESS: single
? TOPOLOGY: linear
? MOLECULE TYPE: protein
? US-09-732-350-8

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Query Match 17.7%; Score 557.5; DB 10; Length 575;
Best Local Similarity 30.9%; Pred. No. 1.1e-39;
Matches 183; Conservative 61; Mismatches 214; Indels 135; Gaps 28;

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QY 44 DNTGPGVYKVKVLYNNSITGPTIPADMGDTIOVTVINNLEFN-----GTSIHWHGLH 98
DB 30 DGEIAPDG-VKRNATLVNGGYPGLIFANKGDTLKVKVQNKLTNPMPYFTTSHHGL 87
QY 99 QKGNLHDGANGITECPFIPKGGKRYRFRKA---QOYGTSMYSHFSAOXNGVGAIOI 155
DB 88 QHRADDGGSFYTGCTIV---RESTYTIPLDDGTGTWYHSHLSQYVDGLRPLVI 144
QY 156 --NGPASPYPYTD--LGVPFISDYSSADEL-----VELTKNSGAPFS-DNVL 199
DB 145 YPKPHRLXVDVDEKTVLLIGDWHYHSSKALLASGNITRQRPVSATINCKGRDPDN-- 202
QY 200 FNGAKHPETGEGEYANVTLPGRHRLRLINISVENHPOVSLVNHFMCIADMPVYNA 259
DB 203 ---TPRPDPT---LYTLKVRKGRYRLRVINSEIASFFSVEGHVTVYIADGVSTKP 255
QY 260 MTVDLSLGVGORYDYVIEANRTPGNTFVNV-----TFGGGLCGGSRNP----- 305
DB 256 YQDAFPIIAGQRIDCVENANQERDWTYINAPLTVNPKTAQALLVYEEERRPRHPKGP 315
QY 306 -----PAALFHY-----AGAPGGPPTD--EGKAPV--DHNCLDLPLNKPVVARD 345
DB 316 YRKMSSEALIKYWNHKKHGRGLLSGHGLKAKMIEGSHLSRSVYKRONETTVVMD 375
QY 346 -----VPLS--GEA---KRAONTLDVTLDT---TGCTPLFVKVNGS-----SAIN 381
DB 376 ESKIVPLEYEGACGSPADVLDTLGTGLNPAIGH---WMINIPYESKPIPLTKILTF 431
QY 382 IDMGRAVDVYLQNTSFPFGYINIVEVNGADQMSYMLIENDPGAFPLPMPMLAGH--D 439
DB 432 DEDGVTSDFKREHYTLPRKNCIEFN-----IKNSGIPIT--HPVHLGHWTMD 480

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QY 440 FYVLGRSPDESPASNERHVEDPARDAGILSGANFVRDVSMLPAFGWVLSFRADNPGAW 499
DB 481 VYQGNPNP-----NYNPRRDVYGSITAG-VRIQFKDNDNGPW 519
QY 500 LFCHIAMHVSGLGVYLLERADDLRGAVSDADAD-DIDRLCADWRRYPTNP 551
DB 520 FLHCHIDWHLEEGFAMVFAEPAEAVKGGPSVAVDSQMEGICGKDYDWLKSNP 572

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## RESULT 9

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US-09-732-350-4
? Sequence 4, Application US/09732350
? Patent No. US20010031490A1
? GENERAL INFORMATION:
? APPLICANT: Svendsen, Allan
? TITLE OF INVENTION: LACCASE MUTANTS
? NUMBER OF SEQUENCES: 10
? CORRESPONDENCE ADDRESS:
? ADDRESSEE: No. US20010031490A1o No. US20010031490A1disk of No. US20010031490
? STREET: 405 Lexington Avenue
? CITY: New York
? STATE: NY
? COUNTRY: USA
? ZIP: 10174
? COMPUTER READABLE FORM:
? MEDIUM TYPE: Diskette
? COMPUTER: IBM Compatible
? OPERATING SYSTEM: DOS
? SOFTWARE: FASTSEQ for Windows Version 2.0
? CURRENT APPLICATION DATA:
? APPLICATION NUMBER: US/09/732,350
? FILING DATE:
? CLASSIFICATION:
? PRIOR APPLICATION DATA:
? APPLICATION NUMBER: 09/032,315
? FILING DATE:
? ATTORNEY/AGENT INFORMATION:
? NAME: Rozek, Carol
? REGISTRATION NUMBER: 36,993
? REFERENCE/DOCKET NUMBER: 5200.200-US
? TELECOMMUNICATION INFORMATION:
? TELEPHONE: 212-867-0123
? TELEFAX: 212-878-9655
? INFORMATION FOR SEQ. ID NO: 4:
? SEQUENCE CHARACTERISTICS:
? LENGTH: 548 amino acids
? TYPE: amino acid
? STRANDEDNESS: single
? TOPOLOGY: linear
? MOLECULE TYPE: protein
? US-09-732-350-4

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Query Match 17.6%; Score 556; DB 10; Length 548;
Best Local Similarity 31.6%; Pred. No. 1.4e-39;
Matches 162; Conservative 66; Mismatches 195; Indels 90; Gaps 22;

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QY 49 PDGVKREKVMLYNNSITGPTIPADMGDTIOVTVINNLEFN-----SIHHHGLHOKGTN 103
DB 38 PDGFSROAV-LAESVFPGPLIAGKNGDFQINVYDEL-TNATYMLKTTTHHGHFGQGTN 95
QY 104 LHDGANGITECPFIPKGGKRYRFRKA---QOYGTSMYSHFSAOXNGVGAIOINGPASP 162
DB 96 WADGPAPINOCPI-ASGDSFLYNNQVDPDQAGTFYHSHLSQYCDGLRGPPVYVDPAD-P 153
QY 163 Y-----DTDLGVFPISDYIYSSADELVELTKNSGAPF--SDNVLFGNGTAKHPETG--EG 212
DB 154 YLDQYDVDDSTVTITLADWYHTAA-----RLGSPFPADTLLINGLGGCGEAGCPVS 205
QY 213 EVANVTLPGRHRLRLINISVENHPOVSLVNHFMCIADMPVYNAVMTVDLSLFGVGR 272
DB 206 DLANVSTKGRKRYRFLVYSICDSFFTFISDGHSLNVEVDATNHQPLTYDELITTYAGOR 265

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OY 325 KA-PVDHNCIDLPNKPVAVADYPLSGFAKARNDTLDTTGTPLTFVKVNGSAINID 383  
DB 315 NNPDAQIENADFLIDPAAPGIPTPG---AADVNLRFQJGFSG----- 355  
OY 384 WGAAYVDYVLTOMTSPPGYNIVEVNGADQMS-----YMLIEND-----PGAPFTL 429  
DB 356 -GFTTNGTAYESPVPPLIQT--MSGAGSANDLLPAGSVYELPRQGVYELVVPAGVLAG 412  
OY 430 PPHMLHGHDFYVLGSGSPDESPASNERHVPDPARDAG--LLSGANPYRDVSMLEPAFG-W 486  
DB 413 PPHFHLHGAFSVY-----RSAGSSRYNNVNPVKRQVSLGTYGDE 433  
OY 487 VVISFRADNFGAMLFCHIAMHVSGLGVYTLERADDLRGAVSDADADDID--RLC 540  
DB 454 VTRFVTDNCGPWFFCHIEFHLMNGIAIVE---AEDMANTV--DANNPVEWMAQLC 505

RESULT 5  
US-09-732-350-5  
Sequence 5, Application US/09732350  
Patent No. US20010031490A1  
GENERAL INFORMATION:  
APPLICANT: Svendsen, Allan  
APPLICANT: Xu, Feng  
TITLE OF INVENTION: LACCASE MUTANTS  
NUMBER OF SEQUENCES: 10  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: No. US20010031490A1o No. US20010031490A1disk of No. US20010031490A1lt  
STREET: 405 Lexington Avenue  
CITY: New York  
STATE: NY  
COUNTRY: USA  
ZIP: 10174  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSeq for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/732,350  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 09/032,315  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Rozek, Carol  
REGISTRATION NUMBER: 36,993  
REFERENCE/DOCKET NUMBER: 5200.200-US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 212-867-0123  
TELEFAX: 212-878-9655  
INFORMATION FOR SEQ ID NO: 5:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 529 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-09-732-350-5

Query Match 19.3%; Score 609.5; DB 10; Length 529;  
Best Local Similarity 30.3%; Pred. No. 3.8e-44;  
Matches 175; Conservative 73; Mismatches 195; Indels 135; Gaps 24;

OY 25 VDSPPGVVPYTLTLEVTNMTGPGVVEKYMALVNSIIGTIPADMGDIQVYINN 84  
DB 14 VSTRPAFAVANKFKDKKNV--VAPDG-FRSDIVSNGVLPGILIRANKDITLRINVTQ 70  
OY 85 LE---TNGTSIMHGLHOKGTMLDGANGITCEP-----IPKGGRRVYRFAK 130  
DB 71 LTDPMSRRATTIMHGLFOATADGPAVFTOCPIAONLSYTYEILPLRG----- 120

OY 131 QYGTSMYSHFSQAQYNGVVAIQI---NGPASIPLYDTD--LGVPFIDSYSSADELVE 185  
DB 121 QGTSMYHAHLAQYDGLGRLVYIDPNBPHSRVDVDASTVWMLDEMYHTPAPVLEK 180  
OY 186 ---LTKNSG--APFSDNVLNFKAKHPEGEGERANVTLP-----GRRHRLIINT 232  
DB 181 QMFSTNNLTALLSPVPPSGLIN-----GKGRYVGGPAVPRSVINWKRKRRLVYINA 232  
OY 233 SVENHFOVSLVNTWCIADNVPMVNAWVDSLEFGVGRYDVVIEANRPGYWFEN--V 290  
DB 233 SAIGSTFTFEGSLIVYIEADGILHQPILAVDSQIYAGQNTSYVZANOTANYMIRAPR 292  
OY 291 TFGGGLCGGSRNPYPA---ALPHYAGAPGPPTDE-----GKAPVHNCIDLPN----- 337  
DB 293 TVAG---AGTNAMLDPTNVFAVLHYEGAPNAEPTTEGSAIGTALVEENLHALINFGAG 349  
OY 338 -----LKPVAVADYPLSGFAKARNDTLDTTGTPLTFVKVNGSAINIDMGRAYV 389  
DB 350 GSAPADVSLMLAIGRST--VDGILRFTFNNIKYEAPSLPTLLKILANNAS-----NDA 400  
OY 390 DYVLTQNTSEPPGYNIVEVN---GADQWYMLIENDPGAPFTLPHHMLHGHDFYV---L 443  
DB 401 DFTPNHETIVLPINKYIELNITGAD-----HHIHLHGHTFVYKSI 442  
OY 444 GRSPDESPASNERHVPDPARDAGLLSGANPYRDVSMLEPAFGVYLSFRADNFGAMLFHC 503  
DB 443 GGPNNV-----VNPFRDVRVVGQTG--VVLRFVTDNCGPWFFVHC 480  
OY 504 HIMHVSGLGVYTLERADDLRGAVSDADADDID--RLC 540  
DB 481 HIDWHLGALVFAEPQOIRQGVQSVOPNNMMDLC 518

RESULT 6  
US-09-732-350-3  
Sequence 3, Application US/09732350  
Patent No. US20010031490A1  
GENERAL INFORMATION:  
APPLICANT: Svendsen, Allan  
APPLICANT: Xu, Feng  
TITLE OF INVENTION: LACCASE MUTANTS  
NUMBER OF SEQUENCES: 10  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: No. US20010031490A1o No. US20010031490A1disk of No. US20010031490A1  
STREET: 405 Lexington Avenue  
CITY: New York  
STATE: NY  
COUNTRY: USA  
ZIP: 10174  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSeq for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/732,350  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 09/032,315  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Rozek, Carol  
REGISTRATION NUMBER: 36,993  
REFERENCE/DOCKET NUMBER: 5200.200-US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 212-867-0123  
TELEFAX: 212-878-9655  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 499 amino acids  
TYPE: amino acid

US-09-732-350-10

Query Match 100.0%; Score 3158; DB 10; Length 573;  
 Best Local Similarity 100.0%; Pred. No. 66-261;  
 Matches 573; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 QOSCNTPSNRACWTDGDIINTDYEVDSPTDGVVRYPTLLTLEVDNMTGPDGVYKEMVLY 60
DB 1 QOSCNTPSNRACWTDGDIINTDYEVDSPTDGVVRYPTLLTLEVDNMTGPDGVYKEMVLY 60
QY 61 NNSIIGPTIFADMGDTIOVYVNNLEFNGTSIMHGHGKGTNLDGANGITECPPIPKG 120
DB 61 NNSIIGPTIFADMGDTIOVYVNNLEFNGTSIMHGHGKGTNLDGANGITECPPIPKG 120
QY 121 GRKYRFAKAOQYGTSMYSHSFAQYGNVGVAIQINGPASLPYDTDLGVPIPSIDYYSSA 180
DB 121 GRKYRFAKAOQYGTSMYSHSFAQYGNVGVAIQINGPASLPYDTDLGVPIPSIDYYSSA 180
QY 181 DELVELTKNSGAPPSDNLVFNKGAKHPETGESEYANVTLPGRHRRLRLINTSVENHFQY 240
DB 181 DELVELTKNSGAPPSDNLVFNKGAKHPETGESEYANVTLPGRHRRLRLINTSVENHFQY 240
QY 241 SLVNHMTCIIAADMVPVNAATVDSLEFGVQORYDVYTEANRTGNYFNVTFGGGLLCGG 300
DB 241 SLVNHMTCIIAADMVPVNAATVDSLEFGVQORYDVYTEANRTGNYFNVTFGGGLLCGG 300
QY 301 SRNPYPAIFHYAGAPGPTDEGKAPVDHNCIDLPLNLRPVVARDVPLSGFAKRAADNTLD 360
DB 301 SRNPYPAIFHYAGAPGPTDEGKAPVDHNCIDLPLNLRPVVARDVPLSGFAKRAADNTLD 360
QY 361 VTLDITGTPTLFWKYNVSAINIDMGRAVVDYVLTONTSPFGGNIYEVNADQMSYWLIE 420
DB 361 VTLDITGTPTLFWKYNVSAINIDMGRAVVDYVLTONTSPFGGNIYEVNADQMSYWLIE 420
QY 421 NDGAPFTLPHPHLHGHDYVYLGSRSPDESPASNERHVFPPARDAGLLSGANPRBRVSM 480
DB 421 NDGAPFTLPHPHLHGHDYVYLGSRSPDESPASNERHVFPPARDAGLLSGANPRBRVSM 480
QY 481 LPAFGWVYLSFRADNPGAMLFCHIAHWYSGGLGVYLLERADDLRGAVSDADADDLDRLC 540
DB 481 LPAFGWVYLSFRADNPGAMLFCHIAHWYSGGLGVYLLERADDLRGAVSDADADDLDRLC 540
QY 541 ADMRRYWPTRPYKPSDGLKHRNVEGEMLYKA 573
DB 541 ADMRRYWPTRPYKPSDGLKHRNVEGEMLYKA 573

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RESULT 2

US-09-732-350-9

Sequence 9, Application US/09732350

Patent No. US20010031490A1

GENERAL INFORMATION:

APPLICANT: Svendsen, Allan

APPLICANT: Xu, Feng

TITLE OF INVENTION: LACCASE MUTANTS

NUMBER OF SEQUENCES: 10

CORRESPONDENCE ADDRESS:

ADDRESSEE: No. US20010031490A10 No. US20010031490A1disk of No. US20010031490A1ch

STREET: 405 Lexington Avenue

CITY: New York

STATE: NY

COUNTRY: USA

ZIP: 10174

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible

OPERATING SYSTEM: DOS

SOFTWARE: FastSeq for Windows Version 2.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/732,350

FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 09/032,315  
 FILING DATE:  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Rozek, Carol  
 REGISTRATION NUMBER: 36,993  
 REFERENCE/DOCKET NUMBER: 5200, 200-US  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 212-867-0123  
 TELEFAX: 212-878-9655  
 INFORMATION FOR SEQ ID NO: 9:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 616 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 US-09-732-350-9

Query Match 65.8%; Score 2076.5; DB 10; Length 616;  
 Best Local Similarity 66.8%; Pred. No. 7e-169;  
 Matches 380; Conservative 66; Mismatches 116; Indels 7; Gaps 6;

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QY 1 QOSCNTPSNRACWTDGDIINTDYEVDSPTDGVVRYPTLLTLEVDNMTGPDGVYKEMVLY 60
DB 1 QOSCNTPSNRACWTDGDIINTDYEVDSPTDGVVRYPTLLTLEVDNMTGPDGVYKEMVLY 60
QY 61 NNSIIGPTIFADMGDTIOVYVNNLEFNGTSIMHGHGKGTNLDGANGITECPPIPKG 120
DB 61 NNSIIGPTIFADMGDTIOVYVNNLEFNGTSIMHGHGKGTNLDGANGITECPPIPKG 120
QY 107 NDRLGTPVFNKMDTTEVYVNNHNRKNGTSIMHGHGKGTNLDGANGITECPPIPKG 165
DB 107 NDRLGTPVFNKMDTTEVYVNNHNRKNGTSIMHGHGKGTNLDGANGITECPPIPKG 165
QY 121 GRKYRFAKAOQYGTSMYSHSFAQYGNVGVAIQINGPASLPYDTDLGVPIPSIDYYSSA 180
DB 121 GRKYRFAKAOQYGTSMYSHSFAQYGNVGVAIQINGPASLPYDTDLGVPIPSIDYYSSA 180
QY 166 GSRYVSPRAROYGTSMYSHSFAQYGNVGVAIQINGPASLPYDTDLGVPIPSIDYYSSA 225
DB 166 GSRYVSPRAROYGTSMYSHSFAQYGNVGVAIQINGPASLPYDTDLGVPIPSIDYYSSA 225
QY 181 DELVELTKNSGAPPSDNLVFNKGAKHPETGESEYANVTLPGRHRRLRLINTSVENHFQ 239
DB 181 DELVELTKNSGAPPSDNLVFNKGAKHPETGESEYANVTLPGRHRRLRLINTSVENHFQ 239
QY 226 DQVLETPKNGAPPSDNLVFNKGAKHPETGESEYANVTLPGRHRRLRLINTSVENHFQ 285
DB 226 DQVLETPKNGAPPSDNLVFNKGAKHPETGESEYANVTLPGRHRRLRLINTSVENHFQ 285
QY 240 VSLVNHMTCIIAADMVPVNAATVDSLEFGVQORYDVYTEANRTGNYFNVTFGGGLLCGG 299
DB 240 VSLVNHMTCIIAADMVPVNAATVDSLEFGVQORYDVYTEANRTGNYFNVTFGGGLLCGG 299
QY 286 VSLAKHMTVYLAADMVPVNAATVDSLEFGVQORYDVYTEANRTGNYFNVTFGGGLLCGG 345
DB 286 VSLAKHMTVYLAADMVPVNAATVDSLEFGVQORYDVYTEANRTGNYFNVTFGGGLLCGG 345
QY 300 GSNNPYPAIFHYAGAPGPTDEGKAPVDHNCIDLPLNLRPVVARDVPLSGFAKRAADNTLD 359
DB 300 GSNNPYPAIFHYAGAPGPTDEGKAPVDHNCIDLPLNLRPVVARDVPLSGFAKRAADNTLD 359
QY 346 FSHNPAPALFRYEGADALPTDGAAPKDHQCDTLDLSPVQKNPVQGFVYEPGNTL 405
DB 346 FSHNPAPALFRYEGADALPTDGAAPKDHQCDTLDLSPVQKNPVQGFVYEPGNTL 405
QY 360 DVTL--DTTGP--LFWKYNVSAINIDMGRAVVDYVLTONTSPFGGNIYEVNADQMSYWLIE 415
DB 360 DVTL--DTTGP--LFWKYNVSAINIDMGRAVVDYVLTONTSPFGGNIYEVNADQMSYWLIE 415
QY 406 PVLHVDQAAAPHVFTWKINGSDADVDMDRVLLEYVANNNDLSIPVKNNTIVRVDGVNEMT 465
DB 406 PVLHVDQAAAPHVFTWKINGSDADVDMDRVLLEYVANNNDLSIPVKNNTIVRVDGVNEMT 465
QY 416 YMLIENDPGAPFTLPHPHLHGHDYVYLGSRSPDESPASNERHVFPPARDAGLLSGANPRBRV 475
DB 416 YMLIENDPGAPFTLPHPHLHGHDYVYLGSRSPDESPASNERHVFPPARDAGLLSGANPRBRV 475
QY 466 YMLIENDPGAPFTLPHPHLHGHDYVYLGSRSPDESPASNERHVFPPARDAGLLSGANPRBRV 525
DB 466 YMLIENDPGAPFTLPHPHLHGHDYVYLGSRSPDESPASNERHVFPPARDAGLLSGANPRBRV 525
QY 476 RDVSMALPFGWVYLSFRADNPGAMLFCHIAHWYSGGLGVYLLERADDLRGAVSDADADD 535
DB 476 RDVSMALPFGWVYLSFRADNPGAMLFCHIAHWYSGGLGVYLLERADDLRGAVSDADADD 535
QY 526 RDVYMLPARGLLALFRTDNGAMLFCHIAHWYSGGLGVYLLERADDLRGAVSDADADD 585
DB 526 RDVYMLPARGLLALFRTDNGAMLFCHIAHWYSGGLGVYLLERADDLRGAVSDADADD 585
QY 536 LDRICADMRRYWPTRPYKPSDGLKHRNVEGEMLYKA 563
DB 536 LDRICADMRRYWPTRPYKPSDGLKHRNVEGEMLYKA 563
QY 586 LERVCREMKDWEAKSPHGKIDSGLKRRW 614
DB 586 LERVCREMKDWEAKSPHGKIDSGLKRRW 614

```

RESULT 3

US-09-732-350-2

Sequence 2, Application US/09732350

Patent No. US20010031490A1

GENERAL INFORMATION:

APPLICANT: Svendsen, Allan

APPLICANT: Xu, Feng

TITLE OF INVENTION: LACCASE MUTANTS

NUMBER OF SEQUENCES: 10

CORRESPONDENCE ADDRESS:

```

Db 228 DELVELTKNSGAFESDNVLENGTAKHPETGECEYANVTLPGRHRRLRLINTSEVNHQY 287
QY 241 SLVNHMTCTIADAMVPVNAATVDSLFLGVRDYVIEANRTPGNWYFPGGLGCG 300
Db 288 SLVNHMTCTIADAMVPVNAATVDSLFLGVRDYVIEANRTPGNWYFPGGLGCG 347
QY 301 SRNPYPAALFHYAGAPGPTDEGKAPVDHNCIDLPLKRPVAVADYPLSGFAKADNTLD 360
Db 348 SRNPYPAALFHYAGAPGPTDEGKAPVDHNCIDLPLKRPVAVADYPLSGFAKADNTLD 407
QY 361 VILDTGTGTLFVWKVNGSAINIDMGRAVVDYVLTQNTSPPPGYNIYEYNGADQWSTWLE 420
Db 408 VILDTGTGTLFVWKVNGSAINIDMGRAVVDYVLTQNTSPPPGYNIYEYNGADQWSTWLE 467
QY 421 NDGPAFTLPHPMHLHGHPFYVYLGSRPDESPASNERHVPDPADAGLLSGANFVRDYSM 480
Db 468 NDGPAFTLPHPMHLHGHPFYVYLGSRPDESPASNERHVPDPADAGLLSGANFVRDYSM 527
QY 481 LPAFGWVLSFRADNPGAMLFCHIAMHVSGLGVYVYLERADDLRGAVSDADADDLRLC 540
Db 528 LPAFGWVLSFRADNPGAMLFCHIAMHVSGLGVYVYLERADDLRGAVSDADADDLRLC 587
QY 541 ADMRRYPTNPYPKSDSGLKHRRVEGEMLYKA 573
Db 588 ADMRRYPTNPYPKSDSGLKHRRVEGEMLYKA 620

RESULT 15
US-08-749-882A-2
; Sequence 2, Application US/08749882A
; Patent No. 5750388
; GENERAL INFORMATION:
; APPLICANT: Berka, Randy
; APPLICANT: Thompson, Sheryl
; APPLICANT: Xu, Teng
; TITLE OF INVENTION: Purified Scytalidium Laccases
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 57503880 No. 5750388disk Of No. 5750388th America, Inc.
; STREET: 405 Lexington Avenue - 64th Fl.
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10174
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FASTSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/749,882A
; FILING DATE: 15-NOV-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Lambiris, Elias J
; REGISTRATION NUMBER: 33,728
; REFERENCE/DOCKET NUMBER: 4186,020-US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-878-9652
; TELEFAX: 212-878-9655
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 616 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; ORIGINAL SOURCE:
; ORGANISM: Scytalidium thermophilum
; US-08-749-882A-2

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Query Match

66.2%; Score 2089.5; DB 1; length 616;

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Best Local Similarity 67.0%; Pred. No. 56-189;
Matches 381; Conservative 66; Mismatches 115; Indels 7; Gaps 6;
QY 1 QOSCNTPSNRACCTDQIDINTDYEDVSDPOTGVYRPTLLILEEDNMTGPDGVYKEVMY 60
Db 47 QGCHSPSNRACWCSCGFINTDYEKTPTNPGVRRRTFTITVEDNRPDGVYKEVMY 106
QY 61 NSIIIGPTFADMGDTIQVTVINLTNCTSIHWHGKHOKGTLLHKGANGITCEPIPPKG 120
Db 107 NDKLGPFTVPAKMGDTIETVANNHLLNTNSTIHHGKHOKGTLLHKGANGITCEPIPPKG 165
QY 121 GRRVYRPAKQOYGTQVYSHSFSAQYNGVGAIOINGPASPYPDTDLGVFPISDYYS 180
Db 166 GSRVYRPAKQOYGTQVYSHSFSAQYNGVGAIOINGPASPYPDTDLGVFPISDYYS 225
QY 181 DELV-ELTKNSGAFESDNVLENGTAKHPETGECEYANVTLPGRHRRLRLINTSEVNHQY 239
Db 226 DQVLTETLAKGNAPEFSDNVLINGTAKHPETGECEYANVTLPGRHRRLRLINTSEVNHQY 285
QY 240 VSLVNHMTCTIADAMVPVNAATVDSLFLGVRDYVIEANRTPGNWYFPGGLGCG 299
Db 286 VSLVNHMTCTIADAMVPVNAATVDSLFLGVRDYVIEANRTPGNWYFPGGLGCG 345
QY 300 GSRNPYPAALFHYAGAPGPTDEGKAPVDHNCIDLPLKRPVAVADYPLSGFAKADNTLD 359
Db 346 FSHNPAPAAIFRYEGAPDALPTDPAAPKRDHCLDTLIDLSPPVQKNVPDVGFEVKEBENTL 405
QY 360 DVTLL-DTGTGTLFVWKVNGSAINIDMGRAVVDYVLTQNTSPPPGYNIYEYNGADQW 415
Db 406 PVTLVHVDQAAAPVFTWTKNGSADVDMDRPALEYVNNNDLSIPVKNMIVRQVGNENMT 465
QY 416 YMLIENDPGAPFTLPHPMHLHGHPFYVYLGSRPDESPASNERHVPDPADAGLLSGANPYR 475
Db 466 YMLIENDPGAPFTLPHPMHLHGHPFYVYLGSRPDESPASNERHVPDPADAGLLSGANPYR 525
QY 476 RDVSMPLPAGWVLSFRADNPGAMLFCHIAMHVSGLGVYVYLERADDLRGAVSDADADD 535
Db 526 RDVSMPLPAGWVLSFRADNPGAMLFCHIAMHVSGLGVYVYLERADDLRGAVSDADADD 585
QY 536 LDRICADWRRYPTNPYPKSDSGLK-HRW 563
Db 586 LDRICADWRRYPTNPYPKSDSGLK-HRW 614

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Search completed: December 4, 2002, 10:48:03  
 Job time : 19 secs



COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/576,281  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/993,318  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Greeng, Valeta A.  
REGISTRATION NUMBER: 33,728  
REFERENCE/DOCKET NUMBER: 5032.200-US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 212-867-0123  
TELEFAX: 212-878-9655  
TELEX:  
INFORMATION FOR SEQ ID NO: 10:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 573 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-09-576-281.10

Query Match 100.0%; Score 3158; DB 4; Length 573;  
Best Local Similarity 100.0%; Pred. No. 3.6e-290;  
Matches 573; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QOSCNTPSNRACWTDGYDINTDYEVDSPTDGVVRYTLTLEVDNMTGPDGVYKXVLY 60  
DB 1 QOSCNTPSNRACWTDGYDINTDYEVDSPTDGVVRYTLTLEVDNMTGPDGVYKXVLY 60  
QY 61 NNSLTGPTIRADMGDTTQVYVNNLENTGSIHWHGKHOKGTNLDHANGITTECPDIPPKG 120  
DB 61 NNSLTGPTIRADMGDTTQVYVNNLENTGSIHWHGKHOKGTNLDHANGITTECPDIPPKG 120  
QY 121 GRKYRRAKAOYGTSMYHSFSAOYGVGAGIINGPASPYPYTDLGVPFISDYSSA 180  
DB 121 GRKYRRAKAOYGTSMYHSFSAOYGVGAGIINGPASPYPYTDLGVPFISDYSSA 180  
QY 181 DEVELTKNSGAPSDNVLENGTAKHPTGEGEYANTLTGRRHRLRLINTSVENHFOY 240  
DB 181 DEVELTKNSGAPSDNVLENGTAKHPTGEGEYANTLTGRRHRLRLINTSVENHFOY 240  
QY 241 SLVNHMCIIAADVPVNAIVDSLEFLGVGQRYDVILEANTPGNYFNVTFFGGLLCGG 300  
DB 241 SLVNHMCIIAADVPVNAIVDSLEFLGVGQRYDVILEANTPGNYFNVTFFGGLLCGG 300  
QY 301 SRNYPALIFHYAGAPGPTDEGKAPVDHNCIDLPLKPYVADVPLSGFAKRAADNTLD 360  
DB 301 SRNYPALIFHYAGAPGPTDEGKAPVDHNCIDLPLKPYVADVPLSGFAKRAADNTLD 360  
QY 361 VTLDTTGTPLFVWKVNGSAINIDMGRAVVDVLTQNTSFPFGYNIIVEVNGADQMSYMLE 420  
DB 361 VTLDTTGTPLFVWKVNGSAINIDMGRAVVDVLTQNTSFPFGYNIIVEVNGADQMSYMLE 420  
QY 421 NDPCAPTLPHMLHGHDFVLGRSPDESASNERHVEDARAGLLSGANPRROYSM 480  
DB 421 NDPCAPTLPHMLHGHDFVLGRSPDESASNERHVEDARAGLLSGANPRROYSM 480  
QY 481 LPAIGWVLSFRADNPGAMLEFCHIAHVSGLGVYLERADDLKGAVSDADADDLRLC 540  
DB 481 LPAIGWVLSFRADNPGAMLEFCHIAHVSGLGVYLERADDLKGAVSDADADDLRLC 540  
QY 541 ADMRRYPTNPKSDGSLKRWVEEGEMLYKA 573  
DB 541 ADMRRYPTNPKSDGSLKRWVEEGEMLYKA 573

RESULT 9

US-08-706-037-27  
Sequence 27, Application US/08706037  
Patent No. 5770419  
GENERAL INFORMATION:  
APPLICANT: Xu, Feng  
APPLICANT: Berka, Randy M.  
APPLICANT: Wahlechner, Jill A.  
TITLE OF INVENTION: BLUE COPPER OXIDASE MUTANTS WITH  
NUMBER OF SEQUENCES: 29  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: No. 5770419 No. 5770419disk of No. 5770419th America, Inc.  
STREET: 405 Lexington Avenue, 64th floor  
CITY: New York  
STATE: New York  
COUNTRY: United States of America  
ZIP: 10174-6401  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/706,037  
FILING DATE: 30-Aug-1996  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 60/002,800  
FILING DATE: 1-Sep-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Harrington, James J.  
REGISTRATION NUMBER: 38,711  
REFERENCE/DOCKET NUMBER: 4526.200-US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 212-867-0123  
TELEFAX: 212-878-9655  
INFORMATION FOR SEQ ID NO: 27:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 620 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-706-037-27

Query Match 100.0%; Score 3158; DB 1; Length 620;  
Best Local Similarity 100.0%; Pred. No. 4e-290;  
Matches 573; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QOSCNTPSNRACWTDGYDINTDYEVDSPTDGVVRYTLTLEVDNMTGPDGVYKXVLY 60  
DB 48 QOSCNTPSNRACWTDGYDINTDYEVDSPTDGVVRYTLTLEVDNMTGPDGVYKXVLY 107  
QY 61 NNSLTGPTIRADMGDTTQVYVNNLENTGSIHWHGKHOKGTNLDHANGITTECPDIPPKG 120  
DB 108 NNSLTGPTIRADMGDTTQVYVNNLENTGSIHWHGKHOKGTNLDHANGITTECPDIPPKG 167  
QY 121 GRKYRRAKAOYGTSMYHSFSAOYGVGAGIINGPASPYPYTDLGVPFISDYSSA 180  
DB 168 GRKYRRAKAOYGTSMYHSFSAOYGVGAGIINGPASPYPYTDLGVPFISDYSSA 227  
QY 181 DEVELTKNSGAPSDNVLENGTAKHPTGEGEYANTLTGRRHRLRLINTSVENHFOY 240  
DB 228 DEVELTKNSGAPSDNVLENGTAKHPTGEGEYANTLTGRRHRLRLINTSVENHFOY 287  
QY 241 SLVNHMCIIAADVPVNAIVDSLEFLGVGQRYDVILEANTPGNYFNVTFFGGLLCGG 300  
DB 288 SLVNHMCIIAADVPVNAIVDSLEFLGVGQRYDVILEANTPGNYFNVTFFGGLLCGG 347  
QY 301 SRNYPALIFHYAGAPGPTDEGKAPVDHNCIDLPLKPYVADVPLSGFAKRAADNTLD 360  
DB 348 SRNYPALIFHYAGAPGPTDEGKAPVDHNCIDLPLKPYVADVPLSGFAKRAADNTLD 407  
QY 361 VTLDTTGTPLFVWKVNGSAINIDMGRAVVDVLTQNTSFPFGYNIIVEVNGADQMSYMLE 420

QY 541 ADMRRYPTNPKSDSGLKHRRVEEGEWLVKA 573  
DB 541 ADMRRYPTNPKSDSGLKHRRVEEGEWLVKA 573

RESULT 5  
US-09-399-866-10  
Sequence 10, Application US/09399886  
Patent No. 6140092  
GENERAL INFORMATION:  
APPLICANT: Pedersen, Anders  
APPLICANT: Svendsen, Allan  
APPLICANT: Schneider, Palle  
APPLICANT: Rasmussen, Grethe  
APPLICANT: Cherry, Joel  
TITLE OF INVENTION: LACCASE MUTANTS  
NUMBER OF SEQUENCES: 10  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: No. 61400920 No. 6140092disk of No. 61400922th America  
STREET: 405 Lexington Avenue  
CITY: New York  
COUNTRY: USA  
ZIP: 10174  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/399,886  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/993,318  
FILING DATE: December 18, 1997  
ATTORNEY/AGENT INFORMATION:  
NAME: Gregg, Valera A.  
REGISTRATION NUMBER: 33,728  
REFERENCE/DOCKET NUMBER: 5032.200-US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 212-867-0123  
TELEFAX: 212-878-9655  
TELEX:  
INFORMATION FOR SEQ ID NO: 10:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 573 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-09-399-866-10

Query Match 100.0%; Score 3158; DB 4; Length 573;  
Best Local Similarity 100.0%; Pred. No. 3.6e-290;  
Matches 573; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QOSCNTPSNRACWTGIDYDINTDYEVDSPDTGVVRYPTLTLEVDNMTGPDGVYKEMVLY 60  
DB 1 QOSCNTPSNRACWTGIDYDINTDYEVDSPDTGVVRYPTLTLEVDNMTGPDGVYKEMVLY 60

QY 61 NNSIIGPTFADMGDTIQTVINNLKNGTSHMHGLHOKGNLHDCANGITECPIDPKG 120  
DB 61 NNSIIGPTFADMGDTIQTVINNLKNGTSHMHGLHOKGNLHDCANGITECPIDPKG 120

QY 121 GKKVYRFAKQOYGTSWYSHFSAOYGNVYGAQINGPASTLPYDTDLGVPIIDYYSSA 180  
DB 121 GKKVYRFAKQOYGTSWYSHFSAOYGNVYGAQINGPASTLPYDTDLGVPIIDYYSSA 180

QY 181 DELVELTKNSGAFSDNVLKNGTAKHPETGEGEVANVTLPGRHRRLRLINTSVENHFOY 240  
DB 181 DELVELTKNSGAFSDNVLKNGTAKHPETGEGEVANVTLPGRHRRLRLINTSVENHFOY 240

QY 241 SLVNHMCIADAMVPMATVDSLFLGVGQRDVIYIENRTGNTWYFNTFGGGLCGG 300

DB 241 SLVNHMCIADAMVPMATVDSLFLGVGQRDVIYIENRTGNTWYFNTFGGGLCGG 300  
QY 301 SRNYPFAIFHYAGAPGPPDEKAPVDHNCIDLPHLKYVAVDVLSGFAKADTLD 360  
DB 301 SRNYPFAIFHYAGAPGPPDEKAPVDHNCIDLPHLKYVAVDVLSGFAKADTLD 360

QY 361 VTLDTTCTPLFVWKVNSAINIDMGRAVVDVLTQNTSFPFGYIVVNGADQSYLIE 420  
DB 361 VTLDTTCTPLFVWKVNSAINIDMGRAVVDVLTQNTSFPFGYIVVNGADQSYLIE 420

QY 421 NDCGAPTLPHPHLHGHDFYVLGRSPDESASNERHVPDPADAGLLSGANPYRDVSM 480  
DB 421 NDCGAPTLPHPHLHGHDFYVLGRSPDESASNERHVPDPADAGLLSGANPYRDVSM 480

QY 481 LPAGWVLSFRADNPPAMLFHCHIAHNVSGGLGVYLERADDLRGAVSDADDLRLC 540  
DB 481 LPAGWVLSFRADNPPAMLFHCHIAHNVSGGLGVYLERADDLRGAVSDADDLRLC 540

QY 541 ADMRRYPTNPKSDSGLKHRRVEEGEWLVKA 573  
DB 541 ADMRRYPTNPKSDSGLKHRRVEEGEWLVKA 573

RESULT 6  
US-09-396-260-10  
Sequence 10, Application US/09396260  
Patent No. 6184015  
GENERAL INFORMATION:  
APPLICANT: Svendsen, Allan  
APPLICANT: Xu, Feng  
TITLE OF INVENTION: LACCASE MUTANTS  
NUMBER OF SEQUENCES: 10  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: No. 61840150 No. 6184015disk of No. 6184015th America, Inc.  
STREET: 405 Lexington Avenue  
CITY: New York  
STATE: NY  
COUNTRY: USA  
ZIP: 10174  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSeq for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/396,260  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/09/032,315  
FILING DATE: 27-FEB-1998  
ATTORNEY/AGENT INFORMATION:  
NAME: Rozek, Carol  
REGISTRATION NUMBER: 36,993  
REFERENCE/DOCKET NUMBER: 5200.200-US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 212-867-0123  
TELEFAX: 212-878-9655  
INFORMATION FOR SEQ ID NO: 10:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 573 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-09-396-260-10

Query Match 100.0%; Score 3158; DB 4; Length 573;  
Best Local Similarity 100.0%; Pred. No. 3.6e-290;  
Matches 573; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QOSCNTPSNRACWTGIDYDINTDYEVDSPDTGVVRYPTLTLEVDNMTGPDGVYKEMVLY 60

```

Db 1 QOQCNTPSNRACWTGDIIDTDEVDSPDGVRRPYTLTLEVDNMTGPGGVKEXMVLV 60
QY 61 NNSIIGFTTADMGDTIOYVIVNNLENGTSHMHGJHOKGTMJHDGANGITECP1PPKG 120
Db 61 NNSIIGFTTADMGDTIOYVIVNNLENGTSHMHGJHOKGTMJHDGANGITECP1PPKG 120
QY 121 GRRVYRKAQOYGTSMYHSHFSAQYGVGAIOINGPASPYPDTDLGVPIISDYSSA 180
Db 121 GRRVYRKAQOYGTSMYHSHFSAQYGVGAIOINGPASPYPDTDLGVPIISDYSSA 180
QY 181 DELVELTKNSGAFPSDNVLENGTAKHPETGEGETANYTLTGRHRRLRLINTSVENHFQY 240
Db 181 DELVELTKNSGAFPSDNVLENGTAKHPETGEGETANYTLTGRHRRLRLINTSVENHFQY 240
QY 241 SLVNHMCIITADMPVPMATVDSLEFLGVGORYDVYEANRTPGNWENYTFGGGLCGG 300
Db 241 SLVNHMCIITADMPVPMATVDSLEFLGVGORYDVYEANRTPGNWENYTFGGGLCGG 300
QY 301 SRNPYPAIFHYAGAPGPTDEGKAPVDHNCIDLPLMKPVADVPLSGFAKADWTLD 360
Db 301 SRNPYPAIFHYAGAPGPTDEGKAPVDHNCIDLPLMKPVADVPLSGFAKADWTLD 360
QY 361 VTLDITGTPLFWKVGNSAINDMGRAVVDYVLTONTSPPGYNIYEVDGADQMSYWLIE 420
Db 361 VTLDITGTPLFWKVGNSAINDMGRAVVDYVLTONTSPPGYNIYEVDGADQMSYWLIE 420
QY 421 NDGAPFTLPHPMHLGHDPYVYGRSPDESPASNERHVPDPADAGLLSGANVRRDYSM 480
Db 421 NDGAPFTLPHPMHLGHDPYVYGRSPDESPASNERHVPDPADAGLLSGANVRRDYSM 480
QY 481 LPAFGWVLSFRADNPGAMLFCHIAHMYSGGLGVYVLEADDLRGAVSPADADDLRLC 540
Db 481 LPAFGWVLSFRADNPGAMLFCHIAHMYSGGLGVYVLEADDLRGAVSPADADDLRLC 540
QY 541 ADMRRYPTNPYRKSGLKHRVVEEGEWLVKA 573
Db 541 ADMRRYPTNPYRKSGLKHRVVEEGEWLVKA 573

```

## RESULT 2

```

US-09-032-315-10
; Sequence 10, Application US/09032315
; Patent No. 5985818
; GENERAL INFORMATION:
; APPLICANT: Svendsen, Allan
; TITLE OF INVENTION: LACCASE MUTANTS
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 59858180 No. 5985818disk of No. 5985818th America, Inc.
; STREET: 405 Lexington Avenue
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10174
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/032, 315
; FILING DATE: 27-FEB-1998
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Roze, Carol
; REGISTRATION NUMBER: 36,993
; REFERENCE/DOCKET NUMBER: 5200, 200-US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-867-0123
; TELEFAX: 212-878-9655
; INFORMATION FOR SEQ ID NO: 10:

```

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; SEQUENCE CHARACTERISTICS:
; LENGTH: 573 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-032-315-10

```

```

Query Match 100.0%; Score 3158; DB 2; Length 573;
Best Local Similarity 100.0%; Pred. No. 3, 6e-290;
Matches 573; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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```

QY 1 QOQCNTPSNRACWTGDIIDTDEVDSPDGVRRPYTLTLEVDNMTGPGGVKEXMVLV 60
Db 1 QOQCNTPSNRACWTGDIIDTDEVDSPDGVRRPYTLTLEVDNMTGPGGVKEXMVLV 60
QY 61 NNSIIGFTTADMGDTIOYVIVNNLENGTSHMHGJHOKGTMJHDGANGITECP1PPKG 120
Db 61 NNSIIGFTTADMGDTIOYVIVNNLENGTSHMHGJHOKGTMJHDGANGITECP1PPKG 120
QY 121 GRRVYRKAQOYGTSMYHSHFSAQYGVGAIOINGPASPYPDTDLGVPIISDYSSA 180
Db 121 GRRVYRKAQOYGTSMYHSHFSAQYGVGAIOINGPASPYPDTDLGVPIISDYSSA 180
QY 181 DELVELTKNSGAFPSDNVLENGTAKHPETGEGETANYTLTGRHRRLRLINTSVENHFQY 240
Db 181 DELVELTKNSGAFPSDNVLENGTAKHPETGEGETANYTLTGRHRRLRLINTSVENHFQY 240
QY 241 SLVNHMCIITADMPVPMATVDSLEFLGVGORYDVYEANRTPGNWENYTFGGGLCGG 300
Db 241 SLVNHMCIITADMPVPMATVDSLEFLGVGORYDVYEANRTPGNWENYTFGGGLCGG 300
QY 301 SRNPYPAIFHYAGAPGPTDEGKAPVDHNCIDLPLMKPVADVPLSGFAKADWTLD 360
Db 301 SRNPYPAIFHYAGAPGPTDEGKAPVDHNCIDLPLMKPVADVPLSGFAKADWTLD 360
QY 361 VTLDITGTPLFWKVGNSAINDMGRAVVDYVLTONTSPPGYNIYEVDGADQMSYWLIE 420
Db 361 VTLDITGTPLFWKVGNSAINDMGRAVVDYVLTONTSPPGYNIYEVDGADQMSYWLIE 420
QY 421 NDGAPFTLPHPMHLGHDPYVYGRSPDESPASNERHVPDPADAGLLSGANVRRDYSM 480
Db 421 NDGAPFTLPHPMHLGHDPYVYGRSPDESPASNERHVPDPADAGLLSGANVRRDYSM 480
QY 481 LPAFGWVLSFRADNPGAMLFCHIAHMYSGGLGVYVLEADDLRGAVSPADADDLRLC 540
Db 481 LPAFGWVLSFRADNPGAMLFCHIAHMYSGGLGVYVLEADDLRGAVSPADADDLRLC 540
QY 541 ADMRRYPTNPYRKSGLKHRVVEEGEWLVKA 573
Db 541 ADMRRYPTNPYRKSGLKHRVVEEGEWLVKA 573

```

## RESULT 3

```

US-08-993-318A-10
; Sequence 10, Application US/08993318A
; Patent No. 5998353
; GENERAL INFORMATION:
; APPLICANT: Pedersen, Anders
; APPLICANT: Svendsen, Allan
; APPLICANT: Schneider, Palle
; APPLICANT: Rasmussen, Grethe
; TITLE OF INVENTION: LACCASE MUTANTS
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 59983530 No. 5998353disk of No. 5998353th America
; STREET: 405 Lexington Avenue
; CITY: New York
; COUNTRY: USA
; ZIP: 10174
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk

```

PT oxidation potential - or altered pH optimum, or mediator or  
 PT oxygen-hydroxide ion pathways, useful for oxidation, for inhibiting  
 PT dye transfer and in bleaching textiles, especially as detergent  
 PT additive  
 PS Claim 15; Page -: 147pp; English.

XX  
 CC The present sequence represents a mutant laccase protein. The  
 CC specification describes active laccase variants (see AAM76282,  
 CC AAM76296-99 and AAM76316-17) having increased oxidation potential,  
 CC altered pH optimum, altered mediator and/or altered oxygen/hydroxide  
 CC ion pathway. The laccase variants are used specifically to oxidise  
 CC substrates, to inhibit dye transfer, and for bleaching textiles,  
 CC specifically denim. They can also be used for lignin modification,  
 CC strengthening paper, polymerisation of phenols, dyeing of hair and  
 CC textiles and waste water treatment.  
 CC note: the present sequence does not appear in the specification; it was  
 CC constructed using information provided.

XX  
 CC Sequence 573 AA;

Query Match 98.5%; Score 3112; DB 19; Length 573;

Best Local Similarity 98.6%; Pred. No. 1, le-271; Mismatches 8; Indels 0; Gaps 0;

Matches 555; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 1 QOSCNTPSNRACWTDGIDTIDYEDSPDGVVRYPTLTLEVDNMTGPDGVYKEMLV 60  
 DB 1 QOSCNTPSNRACWTDGIDTIDYEDSPDGVVRYPTLTLEVDNMTGPDGVYKEMLV 60  
 QY 61 NNSIIGPTFADMGDTIQYVIVNNLENGTSHMHGLOHGTMLHOGANITECP1PPKG 120  
 DB 61 NNSIIGPTFADMGDTIQYVIVNNLENGTSHMHGLOHGTMLHOGANITECP1PPKG 120  
 QY 121 GRKYRFRKAQOYGTSMYSHFSAOYGVNGVGAIOINGPASTLPDITDGVPIEDYYSSA 180  
 DB 121 GRKYRFRKAQOYGTSMYSHFSAOYGVNGVGAIOINGPASTLPDITDGVPIEDYYSSA 180  
 QY 121 GRKYRFRKAQOYGTSMYSHFSAOYGVNGVGAIOINGPASTLPDITDGVPIEDYYSSA 180  
 DB 121 GRKYRFRKAQOYGTSMYSHFSAOYGVNGVGAIOINGPASTLPDITDGVPIEDYYSSA 180  
 QY 181 DELVELTKNSGAPSDNVLEFNGTAKHPETGEGETAVNTLTPGRHRRLRLINTSEVNHFOV 240  
 DB 181 DELVELTKNSGAPSDNVLEFNGTAKHPETGEGETAVNTLTPGRHRRLRLINTSEVNHFOV 240  
 QY 181 DELVELTKNSGAPSDNVLEFNGTAKHPETGEGETAVNTLTPGRHRRLRLINTSEVNHFOV 240  
 DB 181 DELVELTKNSGAPSDNVLEFNGTAKHPETGEGETAVNTLTPGRHRRLRLINTSEVNHFOV 240  
 QY 241 SLVNHMTCTIAADMVNPVNAATVDSLFLVGQRDVYIYAKRTGNTGNTFNTFEGGLCCG 300  
 DB 241 SLVNHMTCTIAADMVNPVNAATVDSLFLVGQRDVYIYAKRTGNTGNTFNTFEGGLCCG 300  
 QY 301 SRNPYPAIPIHYAGAPGPGPTDEGKAPVDHNCIDLPHLKPVVADVPLSGFAKRAVDITLD 360  
 DB 301 SRNPYPAIPIHYAGAPGPGPTDEGKAPVDHNCIDLPHLKPVVADVPLSGFAKRAVDITLD 360  
 QY 361 VILDTGTPTLFWKVNKNSAINIDMGRAVDVYLTONTSEPPGYNIYEVGADQMSYWLIE 420  
 DB 361 VILDTGTPTLFWKVNKNSAINIDMGRAVDVYLTONTSEPPGYNIYEVGADQMSYWLIE 420  
 QY 421 NDGAPPTLPHPHLHGHDYVILGRSPDESASNERHVPAPADAGLLSGANVRRDVS 480  
 DB 421 NDGAPPTLPHPHLHGHDYVILGRSPDESASNERHVPAPADAGLLSGANVRRDVS 480  
 QY 481 LPAFGVWVLSFRADNPGAMLFCHIAMHVSGLGVYVLEBRADLKGAVSDADADDLRLC 540  
 DB 481 LPAFGVWVLSFRADNPGAMLFCHIAMHVSGLGVYVLEBRADLKGAVSDADADDLRLC 540  
 QY 541 ADMRRYWPPTNPYKSDSGLKHRYVEGEEMLVKA 573  
 DB 541 ADMRRYWPPTNPYKSDSGLKHRYVEGEEMLVKA 573

RESULT 15

ID AAM79077 standard; protein; 573 AA.

XX AAM79077;

DT 08-DEC-1998 (first entry)

XX Myceliophthora thermophila laccase mutant.

DE Laccase; mutant; mutagenesis; detergent; bleaching; textile;  
 XX lignin modification; polymerisation; phenol; dyeing.

XX Myceliophthora thermophila.

XX Key Location/Qualifiers

FT Misc-difference 106 /note- "Xaa can be optionally replaced by Ala, Ile,  
 Leu, Phe, Pro, Trp, Tyr, Val"

FT Misc-difference 108 /note- "Xaa can be optionally replaced by Ile, Leu,  
 Phe, Pro, Trp, Tyr, Val"

FT Misc-difference 109 /note- "Xaa can be optionally replaced by Ala, Gln,  
 Ile, Leu, Phe, Pro, Trp, Tyr, Val"

FT Misc-difference 428 /note- "Xaa can be optionally replaced by Ala, Ile,  
 Leu, Phe, Pro, Trp, Tyr, Val"

FT Misc-difference 500 /note- "Xaa can be optionally replaced by Ile, Phe,  
 Trp, Tyr"

FT Misc-difference 510 /note- "Xaa can be optionally replaced by Ala, Ile,  
 Leu, Phe, Pro, Trp, Tyr, Val"

FT Misc-difference 511 /note- "Xaa can be optionally replaced by Ala, Ile,  
 Leu, Phe, Pro, Trp, Tyr, Val"

FT Misc-difference 514 /note- "Xaa can be optionally replaced by Ala, Ile,  
 Leu, Phe, Pro, Trp, Tyr, Val"

FT Misc-difference 514 /note- "Xaa can be optionally replaced by Ala, Ile,  
 Leu, Phe, Pro, Trp, Tyr, Val"

FT Misc-difference 514 /note- "Xaa can be optionally replaced by Ala, Ile,  
 Leu, Phe, Pro, Trp, Tyr, Val"

FT Misc-difference 514 /note- "Xaa can be optionally replaced by Ala, Ile,  
 Leu, Phe, Pro, Trp, Tyr, Val"

FT Misc-difference 514 /note- "Xaa can be optionally replaced by Ala, Ile,  
 Leu, Phe, Pro, Trp, Tyr, Val"

FT Misc-difference 514 /note- "Xaa can be optionally replaced by Ala, Ile,  
 Leu, Phe, Pro, Trp, Tyr, Val"

FT Misc-difference 514 /note- "Xaa can be optionally replaced by Ala, Ile,  
 Leu, Phe, Pro, Trp, Tyr, Val"

FT Misc-difference 514 /note- "Xaa can be optionally replaced by Ala, Ile,  
 Leu, Phe, Pro, Trp, Tyr, Val"

FT Misc-difference 514 /note- "Xaa can be optionally replaced by Ala, Ile,  
 Leu, Phe, Pro, Trp, Tyr, Val"

FT Misc-difference 514 /note- "Xaa can be optionally replaced by Ala, Ile,  
 Leu, Phe, Pro, Trp, Tyr, Val"

FT Misc-difference 514 /note- "Xaa can be optionally replaced by Ala, Ile,  
 Leu, Phe, Pro, Trp, Tyr, Val"

FT Misc-difference 514 /note- "Xaa can be optionally replaced by Ala, Ile,  
 Leu, Phe, Pro, Trp, Tyr, Val"

FT Misc-difference 514 /note- "Xaa can be optionally replaced by Ala, Ile,  
 Leu, Phe, Pro, Trp, Tyr, Val"

FT Misc-difference 514 /note- "Xaa can be optionally replaced by Ala, Ile,  
 Leu, Phe, Pro, Trp, Tyr, Val"

FT Misc-difference 514 /note- "Xaa can be optionally replaced by Ala, Ile,  
 Leu, Phe, Pro, Trp, Tyr, Val"

FT Misc-difference 514 /note- "Xaa can be optionally replaced by Ala, Ile,  
 Leu, Phe, Pro, Trp, Tyr, Val"

FT Misc-difference 514 /note- "Xaa can be optionally replaced by Ala, Ile,  
 Leu, Phe, Pro, Trp, Tyr, Val"

FT Misc-difference 514 /note- "Xaa can be optionally replaced by Ala, Ile,  
 Leu, Phe, Pro, Trp, Tyr, Val"

FT Misc-difference 514 /note- "Xaa can be optionally replaced by Ala, Ile,  
 Leu, Phe, Pro, Trp, Tyr, Val"

FT Misc-difference 514 /note- "Xaa can be optionally replaced by Ala, Ile,  
 Leu, Phe, Pro, Trp, Tyr, Val"

FT Misc-difference 514 /note- "Xaa can be optionally replaced by Ala, Ile,  
 Leu, Phe, Pro, Trp, Tyr, Val"

FT Misc-difference 514 /note- "Xaa can be optionally replaced by Ala, Ile,  
 Leu, Phe, Pro, Trp, Tyr, Val"

FT Misc-difference 514 /note- "Xaa can be optionally replaced by Ala, Ile,  
 Leu, Phe, Pro, Trp, Tyr, Val"

FT Misc-difference 514 /note- "Xaa can be optionally replaced by Ala, Ile,  
 Leu, Phe, Pro, Trp, Tyr, Val"

FT Misc-difference 514 /note- "Xaa can be optionally replaced by Ala, Ile,  
 Leu, Phe, Pro, Trp, Tyr, Val"

FT Misc-difference 514 /note- "Xaa can be optionally replaced by Ala, Ile,  
 Leu, Phe, Pro, Trp, Tyr, Val"

FT Misc-difference 514 /note- "Xaa can be optionally replaced by Ala, Ile,  
 Leu, Phe, Pro, Trp, Tyr, Val"



AC AAW76317;  
 XX 08-JAN-1999 (first entry)  
 DT  
 XX Myceliophthora thermophila-laccase protein variant.  
 DE  
 XX Laccase; variant; oxidation; dye transfer inhibition; bleaching;  
 KM denim; lignin modification; paper strengthening; phenol polymerisation;  
 KW hair dye; waste water treatment.  
 XX  
 OS Synthetic.  
 XX Myceliophthora thermophila.  
 FH Key Location/Qualifiers  
 FT Misc-difference 93 /label= H93E  
 FT /note= "optional"  
 FT Misc-difference 95 /label= H95E  
 FT /note= "optional"  
 FT Misc-difference 109 /label= N109D  
 FT /note= "optional"  
 FT Misc-difference 433 /label= M433E  
 FT /note= "optional"  
 FT Misc-difference 480 /label= M480E  
 FT /note= "optional"  
 FT Misc-difference 506 /label= A506E  
 FT /note= "optional"  
 FT  
 XX W09838287-A1.  
 XX 03-SEP-1998.  
 PD  
 XX 23-FEB-1998; 98WO-DK00070.  
 PF  
 XX 28-FEB-1997; 97DK-0000222.  
 PR  
 XX (NOVO ) NOVO-NORDISK AS.  
 PA  
 XX Svendsen A, Xu F;  
 PI  
 XX  
 DR WPI: 1998-495393/42.  
 XX  
 PT New variants of Coprinus and related laccases with increased  
 PT oxidation potential - or altered pH optimum, or mediator or  
 PT oxygen-hydroxide ion pathways, useful for oxidation, for inhibiting  
 PT dye transfer and in bleaching textiles, especially as detergent  
 PT additive  
 PT  
 XX Claim 18; Page -: 147pp; English.  
 PS  
 XX The present sequence represents a mutant laccase protein. The  
 CC specification describes active laccase variants (see AAW76282,  
 CC AAW76296-99 and AAW76316-17) having increased oxidation potential,  
 CC altered pH optimum, altered mediator and/or altered oxygen/hydroxide  
 CC ion pathway. The laccase variants are used specifically to oxidise  
 CC substrates to inhibit dye transfer, and for bleaching textiles,  
 CC specifically denim. They can also be used for lignin modification,  
 CC strengthening paper, polymerisation of phenols, dyeing of hair and  
 CC textiles and waste water treatment.  
 CC note: the present sequence does not appear in the specification; it was  
 CC constructed using information provided.  
 CC  
 XX Sequence 573 AA:  
 SO  
 Query Match 98.7%; Score 3118; DB 19; Length 573;  
 Best Local Similarity 99.0%; Pred. No. 3.1e-272;  
 Matches 567; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 1 QOSCTFSNRACMTDGYDINTDYEVDSPTGVVRPYTLTTEVDNMTSPDGVEKVALY 60  
 DB 1 QOSCTFSNRACMTDGYDINTDYEVDSPTGVVRPYTLTTEVDNMTSPDGVEKVALY 60  
 QY 61 NNSITIGPTIFADMGDTIOVIVINLETNGTSHHGHLOKGTNLHDGANGITECP1PPKG 120  
 DB 61 NNSITIGPTIFADMGDTIOVIVINLETNGTSHHGHLOKGTNLHDGANGITECP1PPKG 120  
 QY 121 GRKYRREAAQGYGTSWHSHESAQYGNVGAIOINGASLPYOTDLGVPFISDYSSA 180  
 DB 121 GRKYRREAAQGYGTSWHSHESAQYGNVGAIOINGASLPYOTDLGVPFISDYSSA 180  
 QY 181 DELVELTRKNSGAPESDNYLFNGTAKHPETGGEYANWTLTPGRHRLRLTSTVENHPOV 240  
 DB 181 DELVELTRKNSGAPESDNYLFNGTAKHPETGGEYANWTLTPGRHRLRLTSTVENHPOV 240  
 QY 241 SLVNHMCIIAADVPVNAATVDSLFLGVGORYDVIEANPTPGNWFNVTFFGGLLCGG 300  
 DB 241 SLVNHMCIIAADVPVNAATVDSLFLGVGORYDVIEANPTPGNWFNVTFFGGLLCGG 300  
 QY 301 SRNPYPALIFHYAGAPGSPPTDESKAPVDHNCIDLPLKPVAVADVPLSGAKRADWTL 360  
 DB 301 SRNPYPALIFHYAGAPGSPPTDESKAPVDHNCIDLPLKPVAVADVPLSGAKRADWTL 360  
 QY 361 VTLDTGTPLEFVKVNGSAINIDMGRAVDYVLTONTSEPPGYNIVEYNGADOMSYMLIE 420  
 DB 361 VTLDTGTPLEFVKVNGSAINIDMGRAVDYVLTONTSEPPGYNIVEYNGADOMSYMLIE 420  
 QY 421 NDCGAPFTLPHPHLHGDFYVLGRSPDESPASNERHVPDAPDAGLISGANPVRYDSM 480  
 DB 421 NDCGAPFTLPHPHLHGDFYVLGRSPDESPASNERHVPDAPDAGLISGANPVRYDSM 480  
 QY 481 LPFGWVVLSEFRADNPGAMLFHCHIAHVSGLGVYVLEERADDLRGAVSDADADDLRLC 540  
 DB 481 LPFGWVVLSEFRADNPGAMLFHCHIEHVSGLGVYVLEERADDLRGAVSDADADDLRLC 540  
 QY 541 ADMRRYPTNPYPRKSDSGLKRHWEEGEMLYKA 573  
 DB 541 ADMRRYPTNPYPRKSDSGLKRHWEEGEMLYKA 573  
 RESULT 13  
 AAW79078  
 ID AAW79078 standard; protein; 573 AA.  
 XX  
 AC AAW79078;  
 XX  
 XX 08-DEC-1998 (first entry)  
 DT  
 XX Myceliophthora thermophila laccase mutant.  
 DE  
 XX Laccase; mutant; mutagenesis; detergent; bleaching; textile;  
 KM lignin modification; polymerisation; phenol; dyeing.  
 KW  
 XX Myceliophthora thermophila.  
 OS  
 XX  
 FH Key Location/Qualifiers  
 FT Misc-difference 93 /note= "M1d-type His substituted by Glu"  
 FT Misc-difference 95 /note= "M1d-type His substituted by Glu"  
 FT Misc-difference 109 /note= "M1d-type Asn substituted by Asp"  
 FT Misc-difference 433 /note= "M1d-type Met substituted by Glu"  
 FT Misc-difference 480 /note= "M1d-type Met substituted by Glu"  
 FT Misc-difference 506 /note= "M1d-type Met substituted by Glu"  
 FT /note= "M1d-type Ala substituted by Glu"  
 FT  
 XX W09838286-A1.  
 XX 03-SEP-1998.

PA (BERK/) BERKA R M.  
 PA (WAHL/) WAHLEITHNER J A.  
 XX  
 PI Berka RM, Feng X, Wahleithner JA;  
 XX  
 DR WPI; 2000-021805/02.  
 DR N-PSDB; AA224236.  
 XX  
 PT Mutant Rhizoctonia laccase enzymes useful for the polymerization and  
 PT depolymerization of lignin -  
 XX  
 PS Example 9; Column 39-42; 43pp; English.  
 XX  
 CC This invention describes novel mutant Rhizoctonia solani laccase enzymes  
 CC modified to exhibit altered characteristics (e.g. pH activity profile)  
 CC relative to the wild-type enzyme. The mutant enzymes have a number of  
 CC commercial and industrial applications. For example, they may be used for  
 CC the polymerization of lignin (both Kraft and lignosulfates) in solution  
 CC to produce high molecular weight lignin. They may also be used for the in  
 CC situ depolymerization of lignin in Kraft pulp to produce low molecular  
 CC weight lignin. They may also be used for the polymerization of phenolic  
 CC or aniline compounds in liquids (for example apple juice may be treated  
 CC with the enzyme to accelerate precipitation of the phenolic compounds in  
 CC the juice to stabilize it). Additionally, it may be used to decolorize  
 CC dyes and dye precursors by oxidation. The mutant laccase enzymes exhibit  
 CC different characteristics to those of the wild-type enzyme. In  
 CC particular, they may exhibit an altered pH activity profile relative to  
 CC the wild-type enzyme or altered specific activities. Additionally, they  
 CC may be produced in large quantities. This sequence represents the  
 CC Myceliophthora thermophila laccase protein lcc-1.  
 CC  
 XX  
 SQ Sequence 620 AA;

Query Match 100.0%; Score 3158; DB 21; Length 620;  
 Best Local Similarity 100.0%; Pred. No. 8.5e-276;  
 Matches 573; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QOSCTPSNRACMTDGYDINTDYEVDSPDGVVRYTLTLEVDNMTGPGGVKEMLY 60  
 DB 48 QOSCTPSNRACMTDGYDINTDYEVDSPDGVVRYTLTLEVDNMTGPGGVKEMLY 107  
 QY 61 NNSITGPTIADMGDTIQVYVNNLENGTSHHGLHOKGTNLHDGANGTECPIPK 120  
 DB 108 NNSITGPTIADMGDTIQVYVNNLENGTSHHGLHOKGTNLHDGANGTECPIPK 167  
 QY 121 GRKYRKAQOYGSWYSHSFAOYGVGVAIOINGPASPYPDTDLGVEPISDYSSA 180  
 DB 168 GRKYRKAQOYGSWYSHSFAOYGVGVAIOINGPASPYPDTDLGVEPISDYSSA 227  
 QY 181 DELVELTKNSGAPSDVNLFGTAKHPEGTGEYANTLTPGRHRRLRLINTSVENHFQV 240  
 DB 228 DELVELTKNSGAPSDVNLFGTAKHPEGTGEYANTLTPGRHRRLRLINTSVENHFQV 287  
 QY 241 SLVNHMCIIAADMVFNAMATVDSLFGVGRDVTVEANFTPGNTYFNTPFGGLCGG 300  
 DB 288 SLVNHMCIIAADMVFNAMATVDSLFGVGRDVTVEANFTPGNTYFNTPFGGLCGG 347  
 QY 301 SRNYPPIAFHYAGAPGPPDEKAPVDHNCIDLPLMKPVADVPLSGPARADNTLD 360  
 DB 348 SRNYPPIAFHYAGAPGPPDEKAPVDHNCIDLPLMKPVADVPLSGPARADNTLD 407  
 QY 361 VTLDITGTPLEFVKRVNSAINDMGRAVDVYLQNTSPFGYNIIVEGADMSYWLIE 420  
 DB 408 VTLDITGTPLEFVKRVNSAINDMGRAVDVYLQNTSPFGYNIIVEGADMSYWLIE 467  
 QY 421 NDEPAPPTLHPMHLHGHDYVYLGSPDESASMERHVPAPARAGLLSGANPRRVSM 480  
 DB 468 NDEPAPPTLHPMHLHGHDYVYLGSPDESASMERHVPAPARAGLLSGANPRRVSM 527  
 QY 481 LPAFGVVLSPFRADNPGAWLFFCHIAHVSGLGVVLERADDLRGAVSADADDDLRLC 540  
 DB 528 LPAFGVVLSPFRADNPGAWLFFCHIAHVSGLGVVLERADDLRGAVSADADDDLRLC 587

QY 541 ADMRRYPTNPYPKSDSGLRHWEEGEMLYKA 573  
 DB 588 ADMRRYPTNPYPKSDSGLRHWEEGEMLYKA 620  
 RESULT 10  
 ID AAW79079  
 XX AAW79079 standard; protein; 573 AA.  
 AC AAW79079;  
 XX  
 DT 08-DEC-1998 (first entry)  
 XX  
 DE Myceliophthora thermophila laccase mutant.  
 XX  
 KW Laccase; mutant; mutagenesis; detergent; bleaching; textile;  
 XX lignin modification; polymerisation; phenol; dyeing.  
 OS Myceliophthora thermophila.  
 XX  
 FT Key location/qualifiers  
 FT Misc-difference 189  
 FT /note= "Xaa can be optionally replaced by Ala, Gly, Ser,  
 FT Thr"  
 FT Misc-difference 190  
 FT /note= "Xaa can be optionally replaced by Ala, Gly"  
 FT Misc-difference 371  
 FT /note= "Xaa can be optionally deleted or replaced by Ala,  
 FT Gly"  
 FT Misc-difference 218  
 FT label=unknown  
 FT Misc-difference 234  
 FT label=unknown  
 FT Misc-difference 557  
 FT label=unknown  
 PN WO9838286-A1.  
 PD 03-SEP-1998.  
 XX  
 PE 20-FEB-1998; 98WO-DK00067.  
 XX  
 PR 28-FEB-1997; 97DK-0000221.  
 XX  
 PA (NOVO ) NOVO-NORDISK AS.  
 XX  
 PI Svendsen A;  
 XX  
 DR WPI; 1998-495392/42.  
 XX  
 PT New variants of laccase with increased oxidation potential - or  
 PT altered pH optimum, mediator efficiency or oxygen hydroxide ion  
 PT pathways, useful for oxidation, inhibiting dye transfer and in  
 PT textile bleaching  
 PS  
 XX Disclosure; Page -: 34pp; English.  
 XX  
 CC The laccase protein mutants AAW79079 contain one or more of the  
 CC above substitutions and are examples of polypeptides modified from the  
 CC wild-type sequence by using site-directed, random, or localised random  
 CC mutagenesis. These mutants may have an (a) increased oxidation  
 CC potential, (b) altered pH optimum, (c) altered mediator efficiency, (d)  
 CC altered oxygen/hydroxide ion pathway, depending on the particular  
 CC mutations that have occurred. This particular sequence has mutations  
 CC that will alter the laccase's oxygen/hydrogen ion pathway. These  
 CC variants can be used to oxidise substrates, inhibit dye transfer, as  
 CC detergent additives and bleaching textiles. They can also be used in  
 CC lignin modification; strengthening paper; polymerisation of phenols;  
 CC dyeing of hair and textiles and waste water treatment.  
 CC N.B. This sequence is not shown in the specification but is derived  
 CC from the wild-type Myceliophthora thermophila laccase sequence given in  
 CC the specification.

Query Match 100.0%; Score 3158; DB 21; Length 573;  
 Best Local Similarity 100.0%; Pred. No. 7.6e-276;  
 Matches 573; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

QY 1 QQSCNTPSNRACWTDGDIINTDYEVDSPDGVVARYTLTLEVDNMTPGPGVYKEXKMLV 60
DB 1 QQSCNTPSNRACWTDGDIINTDYEVDSPDGVVARYTLTLEVDNMTPGPGVYKEXKMLV 60
QY 61 NNSIIGPTIFADMGDTIQVTVINNLETNGTSIHMHGJHOKGTNLHDGANGITECPPIPKG 120
DB 61 NNSIIGPTIFADMGDTIQVTVINNLETNGTSIHMHGJHOKGTNLHDGANGITECPPIPKG 120
QY 121 GRRVYRKAQOYGTSMYSHSFAQYNGVYGAIDINGPASLPYDTDLGVEPIDSYSSA 180
DB 121 GRRVYRKAQOYGTSMYSHSFAQYNGVYGAIDINGPASLPYDTDLGVEPIDSYSSA 180
QY 181 DELVELTKNSGAPPSDNLNGTAKHPETEGEYANTTLPGRRHRLRLINTSVENHFQY 240
DB 181 DELVELTKNSGAPPSDNLNGTAKHPETEGEYANTTLPGRRHRLRLINTSVENHFQY 240
QY 241 SLVNHPTCIIAADVPVNAATVDSLFLGVGORYDVTEANRTPGNMYFNTPFGGILCGG 300
DB 241 SLVNHPTCIIAADVPVNAATVDSLFLGVGORYDVTEANRTPGNMYFNTPFGGILCGG 300
QY 301 SRNPYPALIFHYAGAPGPPTEDEKAPVDHNCIDLPLMKPVYADVLSGFARADNTLD 360
DB 301 SRNPYPALIFHYAGAPGPPTEDEKAPVDHNCIDLPLMKPVYADVLSGFARADNTLD 360
QY 361 VTLDITGTPLFVWKVNGSAINIDMGRAVDVYLQNTSFPFGYNIIVEANGADQMSYWLIE 420
DB 361 VTLDITGTPLFVWKVNGSAINIDMGRAVDVYLQNTSFPFGYNIIVEANGADQMSYWLIE 420
QY 421 NDGCAPTTLPHPHLHGHDTYVLCRSPDESPASNERHVPFAPDAGILSGANPYRDVSM 480
DB 421 NDGCAPTTLPHPHLHGHDTYVLCRSPDESPASNERHVPFAPDAGILSGANPYRDVSM 480
QY 481 LPAFGVYVLSFRADNPGAMLFHCHIAHVSGLGVYLLERADDLRGAVSDADDDLRLC 540
DB 481 LPAFGVYVLSFRADNPGAMLFHCHIAHVSGLGVYLLERADDLRGAVSDADDDLRLC 540
QY 541 ADMRRYWPNTNYPKSDGSLKRWVEEGEWLYKA 573
DB 541 ADMRRYWPNTNYPKSDGSLKRWVEEGEWLYKA 573

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RESULT 7  
 AAR88500  
 ID AAR88500 standard; Protein; 620 AA.

AC AAR88500;  
 DT 28-MAR-1996 (first entry)  
 XX  
 DE Myceliophthora laccase enzyme.  
 XX  
 KM Laccase; lignin degradation; delignification; depolymerisation;  
 KM Kraft pulp; waste-water; soil detoxification; hair dye;  
 KM hydrogen peroxide.  
 XX  
 OS Myceliophthora thermophila.  
 XX  
 PN WO953836-A1.  
 PD 14-DEC-1995.  
 PF 31-MAY-1995; 95WO-US06815.  
 PR 15-MAY-1995; 95US-0441146.  
 PR 03-JUN-1994; 94US-0253781.  
 XX  
 PA (NOVO ) NOVO NORDISK BIOTECH INC.  
 PA (NOVO ) NOVO-NORDISK AS..  
 XX

PI Aaslyng DA, Berka RM, Brown SH, Oxenboll KM, Schneider P;  
 PI Xu F;  
 XX  
 XX WPI; 1996-058139/06.  
 DR N-PSDB; AAT10922.  
 XX  
 XX DNA encoding a Myceliophthora laccase enzyme - used in hair dye  
 PT compositions, to reduce the use of hydrogen peroxide and improve  
 PT hair condition  
 XX  
 PS Claim 8; Page 41-43; 58pp; English.  
 XX  
 CC The Myceliophthora thermophila laccase (AAR88500) is the product  
 CC of a gene (AAT10922) isolated from a genomic library using the  
 CC Neurospora crassa laccase gene (lcc1) as probe. The enzyme is  
 CC capable of lignin modification, Kraft mill pulp depolymerisation,  
 CC soil detoxification, and of dyeing hair. Recombinant laccase can be  
 CC produced in a prokaryotic or eukaryotic, pref. Aspergillus, host.  
 XX

Sequence 620 AA;

Query Match 100.0%; Score 3158; DB 17; Length 620;  
 Best Local Similarity 100.0%; Pred. No. 8.5e-276;  
 Matches 573; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

QY 1 QQSCNTPSNRACWTDGDIINTDYEVDSPDGVVARYTLTLEVDNMTPGPGVYKEXKMLV 60
DB 48 QQSCNTPSNRACWTDGDIINTDYEVDSPDGVVARYTLTLEVDNMTPGPGVYKEXKMLV 107
QY 61 NNSIIGPTIFADMGDTIQVTVINNLETNGTSIHMHGJHOKGTNLHDGANGITECPPIPKG 120
DB 108 NNSIIGPTIFADMGDTIQVTVINNLETNGTSIHMHGJHOKGTNLHDGANGITECPPIPKG 167
QY 121 GRRVYRKAQOYGTSMYSHSFAQYNGVYGAIDINGPASLPYDTDLGVEPIDSYSSA 180
DB 168 GRRVYRKAQOYGTSMYSHSFAQYNGVYGAIDINGPASLPYDTDLGVEPIDSYSSA 227
QY 181 DELVELTKNSGAPPSDNLNGTAKHPETEGEYANTTLPGRRHRLRLINTSVENHFQY 240
DB 228 DELVELTKNSGAPPSDNLNGTAKHPETEGEYANTTLPGRRHRLRLINTSVENHFQY 287
QY 241 SLVNHPTCIIAADVPVNAATVDSLFLGVGORYDVTEANRTPGNMYFNTPFGGILCGG 300
DB 288 SLVNHPTCIIAADVPVNAATVDSLFLGVGORYDVTEANRTPGNMYFNTPFGGILCGG 347
QY 301 SRNPYPALIFHYAGAPGPPTEDEKAPVDHNCIDLPLMKPVYADVLSGFARADNTLD 360
DB 348 SRNPYPALIFHYAGAPGPPTEDEKAPVDHNCIDLPLMKPVYADVLSGFARADNTLD 407
QY 361 VTLDITGTPLFVWKVNGSAINIDMGRAVDVYLQNTSFPFGYNIIVEANGADQMSYWLIE 420
DB 408 VTLDITGTPLFVWKVNGSAINIDMGRAVDVYLQNTSFPFGYNIIVEANGADQMSYWLIE 467
QY 421 NDGCAPTTLPHPHLHGHDTYVLCRSPDESPASNERHVPFAPDAGILSGANPYRDVSM 480
DB 468 NDGCAPTTLPHPHLHGHDTYVLCRSPDESPASNERHVPFAPDAGILSGANPYRDVSM 527
QY 481 LPAFGVYVLSFRADNPGAMLFHCHIAHVSGLGVYLLERADDLRGAVSDADDDLRLC 540
DB 528 LPAFGVYVLSFRADNPGAMLFHCHIAHVSGLGVYLLERADDLRGAVSDADDDLRLC 587
QY 541 ADMRRYWPNTNYPKSDGSLKRWVEEGEWLYKA 573
DB 588 ADMRRYWPNTNYPKSDGSLKRWVEEGEWLYKA 620

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RESULT 8  
 AAM16302  
 ID AAM16302 standard; Protein; 620 AA.

AC AAM16302;  
 DT 07-AUG-1997 (first entry)  
 XX

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DB 421 NDCPAPFTLPHPHLHGHDEYVLCRSPDESPASNERHVPDPARAGLSCANPVRDYSM 480
OY 481 LPAFGWVLSFRADNPGAMLPHCHIAHWVSGGLGVYLLERADDLRGVADADDLRLC 540
DB 481 LPAFGWVLSFRADNPGAMLPHCHIAHWVSGGLGVYLLERADDLRGVADADDLRLC 540
OY 541 ADMRRWPTNPYPKSDGSLKRWVEEGEMLVKA 573
DB 541 ADMRRWPTNPYPKSDGSLKRWVEEGEMLVKA 573

RESULT 4
AAM51782
ID AAM51782 standard; peptide; 573 AA.
XX
XX AAM51782;
AC
XX 12-OCT-1998 (first entry)
DE Myceliophthora thermophila laccase protein.
XX
XX Laccase protein; variant; lignin modification; paper strengthening;
KM dye transfer inhibition; phenol2 polymerisation; hair dyeing;
KM textile bleaching; denim; waste water treatment.
XX
XX Myceliophthora thermophila.
FH
XX Key Location/Qualifiers
FT misc_difference 136 /note- "optionally replaced with Ala, Val, Leu,
FT Ile, Pro, Phe, Trp, Gly, Ser, Thr, Cys,
FT Tyr, Asn, Gln, Asp, Glu, Lys, Arg or His"
FT misc_difference 137 /note- "optionally replaced with Ala, Val, Leu,
FT Ile, Pro, Phe, Trp, Gly, Ser, Thr, Cys,
FT Tyr, Asn, Gln, Asp, Glu, Lys, Arg or His"
FT misc_difference 145 /note- "optionally replaced with Ala, Val, Leu,
FT Ile, Pro, Phe, Trp, Gly, Ser, Thr, Cys,
FT Tyr, Asn, Gln, Asp, Glu, Lys, Arg or His"
FT misc_difference 176 /note- "optionally replaced with Ala, Val, Leu,
FT Ile, Pro, Phe, Trp, Gly, Ser, Thr, Cys,
FT Tyr, Asn, Gln, Asp, Glu, Lys, Arg or His"
FT misc_difference 254 /note- "optionally replaced with Ala, Val, Leu,
FT Ile, Pro, Phe, Trp, Gly, Ser, Thr, Cys,
FT Tyr, Asn, Gln, Asp, Glu, Lys, Arg or His"
FT misc_difference 373 /note- "optionally replaced with Ala, Val, Leu,
FT Ile, Pro, Phe, Trp, Gly, Ser, Thr, Cys,
FT Tyr, Asn, Gln, Asp, Glu, Lys, Arg or His"
FT misc_difference 433 /note- "optionally replaced with Ala, Val, Leu,
FT Ile, Pro, Phe, Trp, Gly, Ser, Thr, Cys,
FT Tyr, Asn, Gln, Asp, Glu, Lys, Arg or His"
FT misc_difference 480 /note- "optionally replaced with Ala, Val, Leu,
FT Ile, Pro, Phe, Trp, Gly, Ser, Thr, Cys,
FT Tyr, Asn, Gln, Asp, Glu, Lys, Arg or His"
FT misc_difference 507 /note- "optionally replaced with Ala, Val, Leu,
FT Ile, Pro, Phe, Trp, Gly, Ser, Thr, Cys,
FT Tyr, Asn, Gln, Asp, Glu, Lys, Arg or His"

MO9827197-A1.
XX
XX 12-DEC-1997; 97MO-DK00566.
XX
XX 25-JUN-1998.
XX
XX 08-SEP-1997; 97DK-0001020.

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PR 19-DEC-1996; 96DK-0001450.
XX
XX (NOVO ) NOVO-NORDISK AS.
XX
XX Cherry JR, Pedersen AH, Rasmussen G, Schneider P;
PI Svendsen A;
XX
XX WPI; 1998-362767/31.
XX
XX
XX New laccase variants - have amino acid changes in Myceliophthora or
PT Scytalidium laccase(s), used for e.g. oxidation, dye transfer
PT inhibition or bleaching
XX
XX Claim 1; Pages 18-21; 30pp; English.
XX
XX The present sequence represents a laccase protein. The sequence is used
CC to construct laccase variants which have improved stability as compared
CC to the parent laccase, and comprises a mutation in tyrosine, tryptophan
CC or methionine residues. The laccase variants can be used for e.g. lignin
CC modification, paper strengthening, dye transfer inhibition in detergents,
CC phenol polymerisation, hair dyeing, bleaching of textiles (in particular
CC bleaching of denim) and waste water treatment.
XX
XX Sequence 573 AA;
SQ

Query Match 100.0%; Score 3158; DB 19; Length 573;
Best Local Similarity 100.0%; Pred. No. 7.6e-276;
Matches 573; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 QQSCNTSPNRACWTGXDINTDYEDSPDTCGVVRPYTLTLEVDNMTGPDGVREKVMY 60
DB 1 QQSCNTSPNRACWTGXDINTDYEDSPDTCGVVRPYTLTLEVDNMTGPDGVREKVMY 60
OY 61 NNSITGPTIRADMGDTQVYVYNLNLENGTSHHNGGLHOKSTNHDGANGTTECPDPKG 120
DB 61 NNSITGPTIRADMGDTQVYVYNLNLENGTSHHNGGLHOKSTNHDGANGTTECPDPKG 120
OY 121 GRKYRFRKAOYGTSMYSHFSAOYGNVGVAIOINGPASLPYTDGVPFISDYSSA 180
DB 121 GRKYRFRKAOYGTSMYSHFSAOYGNVGVAIOINGPASLPYTDGVPFISDYSSA 180
OY 181 DELVELTKNSGAPPSDNLVLENGTAKHPETGEGEVANTLTGRRHRLRLINTSVENHFQY 240
DB 181 DELVELTKNSGAPPSDNLVLENGTAKHPETGEGEVANTLTGRRHRLRLINTSVENHFQY 240
OY 241 SLVNHMCITIAADVPVNAATVDSLFVGGORGVYVLEANTPCNKENYTFGGGLCGG 300
DB 241 SLVNHMCITIAADVPVNAATVDSLFVGGORGVYVLEANTPCNKENYTFGGGLCGG 300
OY 301 SRNFPYPAIFHYAGAPGPTDEKARVDHNCIDLPLKRPVAVADVPLSGFAKRAADNTLD 360
DB 301 SRNFPYPAIFHYAGAPGPTDEKARVDHNCIDLPLKRPVAVADVPLSGFAKRAADNTLD 360
OY 361 VTLDTGTCTPLFVWKVNSAINIDMGRAVDVYLQNTSFPFGYIVYVNGADQSYTLIE 420
DB 361 VTLDTGTCTPLFVWKVNSAINIDMGRAVDVYLQNTSFPFGYIVYVNGADQSYTLIE 420
OY 421 NDCPAPFTLPHPHLHGHDEYVLCRSPDESPASNERHVPDPARAGLSCANPVRDYSM 480
DB 421 NDCPAPFTLPHPHLHGHDEYVLCRSPDESPASNERHVPDPARAGLSCANPVRDYSM 480
OY 481 LPAFGWVLSFRADNPGAMLPHCHIAHWVSGGLGVYLLERADDLRGVADADDLRLC 540
DB 481 LPAFGWVLSFRADNPGAMLPHCHIAHWVSGGLGVYLLERADDLRGVADADDLRLC 540
OY 541 ADMRRWPTNPYPKSDGSLKRWVEEGEMLVKA 573
DB 541 ADMRRWPTNPYPKSDGSLKRWVEEGEMLVKA 573

RESULT 5
AAM63124
ID AAM63124 standard; peptide; 573 AA.

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Query Match	100.0%	Score 3158	DB 19	Length 573
Best Local Similarity	100.0%	Pred. No. 7.6e-276		
Matches 573	Conservative 0	Mismatches 0	Indels 0	Gaps 0
XX	Disclosure: Pages 133-134; 147pp; English.			
XX	The present sequence represents a laccase protein. The specification			
CC	describes active laccase variants (see AAM76282, AAM76296-99 and			
CC	AAM76316-17) having increased oxidation potential, altered pH optimum,			
CC	altered mediator and/or altered oxygen/hydroxide ion pathway. The			
CC	laccase variants are used specifically to oxidise substrates, to			
CC	inhibit dye transfer, and for bleaching textiles, specifically denim.			
CC	They can also be used for lignin modification, strengthening paper,			
CC	polymerisation of phenols, dyeing of hair and textiles and waste			
CC	water treatment.			
XX	Sequence 573 AA:			
XX				
YY	1 OOSCTPNSRACWGTGVDINTDEYDSDPTGVRRPTLTLTEDNMNTGSDGVKKEVMY 60			
DB	1 QOOSCTPNSRACWGTGVDINTDEYDSDPTGVRRPTLTLTEDNMNTGSDGVKKEVMY 60			
YY	61 NNSIIGPTTFADMGDTIOVTVININLETNGTSHMHGKHOKGTNLHDGANGITECPIPKG 120			
DB	61 NNSIIGPTTFADMGDTIOVTVININLETNGTSHMHGKHOKGTNLHDGANGITECPIPKG 120			
YY	121 GKRVYRFAAOQCTSMYNSHSESAQYGNCGVGAQIQNGRPSLPRDTDLGYFPISDIYSSA 180			
DB	121 GKRVYRFAAOQCTSMYNSHSESAQYGNCGVGAQIQNGRPSLPRDTDLGYFPISDIYSSA 180			
YY	181 DELVELTKNSGAFPSDNVLFNGTAKHPETEGERYANVTLTPGRHRRLRLINTSVENHFOY 240			
DB	181 DELVELTKNSGAFPSDNVLFNGTAKHPETEGERYANVTLTPGRHRRLRLINTSVENHFOY 240			
YY	241 SLVNHNTMCIIADMPVPMAMTVDSLFGLGQRYDYVTEANRPRTGNTWNVTFGGGLICGG 300			
DB	241 SLVNHNTMCIIADMPVPMAMTVDSLFGLGQRYDYVTEANRPRTGNTWNVTFGGGLICGG 300			
YY	301 SNRPRAIFHAGAPGGPPTDEGKAPVDHNCIDLPNLKPVYARQVPLSGPAKPADNTLD 360			
DB	301 SNRPRAIFHAGAPGGPPTDEGKAPVDHNCIDLPNLKPVYARQVPLSGPAKPADNTLD 360			
YY	361 VLTDTTGPRLFVWKVNGSAINIDMGRAVVDYVLTONTSPPEGYNIVEGADQWSYMLE 420			
DB	361 VLTDTTGPRLFVWKVNGSAINIDMGRAVVDYVLTONTSPPEGYNIVEGADQWSYMLE 420			
YY	421 NDGPAPFTLPHMHMLGHDFYVLGNSPDSPSNENHNVDPARADGLLSGAPVPRDYSM 480			
DB	421 NDGPAPFTLPHMHMLGHDFYVLGNSPDSPSNENHNVDPARADGLLSGAPVPRDYSM 480			
YY	481 LPAFGVYVLSFRADNPGAWLFFCHCIAMHVSGGIGVYTERADDLRGAVSDAADDLDRIC 540			
DB	481 LPAFGVYVLSFRADNPGAWLFFCHCIAMHVSGGIGVYTERADDLRGAVSDAADDLDRIC 540			
YY	541 ADMRRYVPTNPYPKSDSGLKHNVVEEGEMLVKA 573			
DB	541 ADMRRYVPTNPYPKSDSGLKHNVVEEGEMLVKA 573			
RESULT 2				
AA55913				
ID	AA55913 standard; protein: 573 AA.			
XX	AA55913;			
XX	08-DEC-1998 (first entry)			
XX	Myceliophthora thermophila laccase protein.			
DE				
XX				
KM	laccase; mutant; mutagenesis; detergent; bleaching; textile;			

xx	Lignin modification; polymerisation; phenol; dyeing.
xx	Mycelophthora thermophila.
os	WO9838286-A1.
pn	03-SEP-1998.
pd	20-FEB-1998;
pf	98WO-DK00067.
pr	28-FEB-1997; 97DK-0000221.
xx	(NOVO ) NOVO-NORDISK AS.
pa	Svendsen A;
pi	WPI; 1998-495392/42.
dr	New variants of laccase with increased oxidation potential - or
pt	altered pH optimum, mediator efficiency or oxygen-hydroxide ion
pt	pathways, useful for oxidation, inhibiting dye transfer and in
pt	textile bleaching
xx	Claim 2; Page 17-20; 34pp; English.
ps	This sequence represents a M. thermophila laccase wild-type polypeptide.
cc	This sequence can be used to generate laccase mutants, by using
cc	site-directed, random, or localised random mutagenesis. These mutants
cc	may have an (a) increased oxidation potential, (b) altered pH optimum,
cc	(c) altered mediator efficiency, (d) altered oxygen/hydroxide ion
cc	pathway, depending on the particular mutations that have occurred. These
cc	variants can be used to oxidise substrates, inhibit dye transfer, as
cc	detergent additives and bleaching textiles. They can also be used in
cc	lignin modification; strengthening paper; polymerisation of phenols;
cc	dyeing of hair and textiles and waste water treatment.
xx	Sequence 573 AA:
s0	Query Match 100.0%; Score 3158; DB 19; Length 573;
	Best Local Similarity 100.0%; Pred. No. 7.6e-276;
	Matches 573; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY	1 QOQCFTPSNRACWDGCIYDINDIYEVDSPTGYVRRPYTLTLEVDNMGTGPGVKKERMLV 60
Db	1 QOQCFTPSNRACWTGDIYDINDIYEVDSPTGYVRPYTLTLEVDNMTGGDGVAKEKVMLY 60
QY	61 NNSIGPITFADMGDTIOVTYNINLETNGTSIHMHGLHOKGNLMDGAGITECPHPKG 120
Db	61 NNSIIIGPITFADMGTIOYTYINMETNGTSHMHGLHOKGNLMDGAGITECIPRKG 120
QY	121 GKRYTRFAQQYGISWYHSFSQAQYGVNGVGAIQINGPASLPDYTDLGVPISIDYYSSA 180
Db	121 GKRVTRFAAQOGISWYHSFSQAQYGVNGVGAIQINGPASLPDYDDLDGFVISDYSSA 180
QY	181 DELVELTFKNSGAFSDNYLFNGTAHPETGESEEVANNLTTPERRRLRLINISVNHHQY 240
Db	181 DELVELTNNSGAFSDNVLFNGTAHPETGESEEVANNTLTTPERRRLRLINISVENHRQY 240
QY	241 SLVNHTEMCITIAADVPPVANMPTVDSLFLGAGQXYDVAVIEANRPXMYWEVNTFGSGLLCGG 300
Db	241 SLVNHTEMCITIAADVPPVANMPTVDSLFLGAGQXYDVAVIEANRPXMYWFVFSGSGLLCGG 300
QY	301 SRNPYPALIFHYAGAPGGPPDEGAAPVDHNCCLDPLNKPVVARDPVLISGFPAKRADNTLD 360
Db	301 SRNPYPALIFHYAGAPGGPPDEGAAPVDHNCCLDPLNKPVVARDPVPLISGFPAKRADNTLD 360
QY	361 VTLDTTGATLEFWKNKNSAINIDMGRAVVYDLTONTSFSPPCYNIVEVNGADOMSTYLIE 420
Db	361 VTLDTTGATLEFWKNKNSAINIDMGRAVVYDLTONTSEFPPCYNIVEVNGADOMSTYLIE 420
QY	421 NDGPAPFLPLPRPMHLHGHDIFYVLGSPPDESASNERHVPDPARDAGLLSGANPVARDYSM 480
Db	421 NDGPAPFLPLPRPMHLHGHDIFYVLGSPPDESASNSRHRVFDPRDAGLLSGANPVARDYSM 480